**PCT** WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : A61K 39/00, 39/29, C07K 7/00, 14/02, 14/82 — A1

(11) International Publication Number: **WO 99/45954**

(43) International Publication Date: 16 September 1999 (16.09.99)

(21) International Application Number: PCT/US98/05039

(22) International Filing Date: 13 March 1998 (13.03.98)

(71) Applicant: EPIMMUNE, INC. [US/US]; Suite 200, 655 Nancy Ridge Drive, San Diego, CA 92121 (US).

(72) Inventors: SETTE, Alessandro; 5551 Linda Rosa Avenue, La Jolla, CA 92037 (US). KUBO, Ralph, T.; 12635 Futura Street, San Diego, CA 92130 (US). SIDNEY, John; 8541 D. Villa La Jolla Drive, La Jolla, CA 92037 (US). CELIS, Esteban; 13644 Landfair Road, San Diego, CA 92130 (US). GREY, Howard, M.; 9066 La Jolla Street, La Jolla, CA 92037 (US). SOUTHWOOD, Scott; 10679 Strathmore Drive, Santee, CA 92071 (US).

(74) Agents: BASTIAN, Kevin, L. et al.; Townsend and Townsend and Crew LLP, 8th floor, Two embarcadero Center, San Francisco, CA 94111–3834 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

**Published**
*With international search report.*

(54) Title: HLA–BINDING PEPTIDES AND THEIR USES

(57) Abstract

The present invention provides the means and methods for selecting immunogenic peptides and the immunogenic peptide compositions capable of specifically binding glycoproteins encoded by HLA allele and inducing T cell activation in T cells restricted by the allele. The peptides are useful to elicit an immune response against a desired antigen.

*FOR THE PURPOSES OF INFORMATION ONLY*

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| AL | Albania | ES | Spain | LS | Lesotho | SI | Slovenia |
| AM | Armenia | FI | Finland | LT | Lithuania | SK | Slovakia |
| AT | Austria | FR | France | LU | Luxembourg | SN | Senegal |
| AU | Australia | GA | Gabon | LV | Latvia | SZ | Swaziland |
| AZ | Azerbaijan | GB | United Kingdom | MC | Monaco | TD | Chad |
| BA | Bosnia and Herzegovina | GE | Georgia | MD | Republic of Moldova | TG | Togo |
| BB | Barbados | GH | Ghana | MG | Madagascar | TJ | Tajikistan |
| BE | Belgium | GN | Guinea | MK | The former Yugoslav Republic of Macedonia | TM | Turkmenistan |
| BF | Burkina Faso | GR | Greece | | | TR | Turkey |
| BG | Bulgaria | HU | Hungary | ML | Mali | TT | Trinidad and Tobago |
| BJ | Benin | IE | Ireland | MN | Mongolia | UA | Ukraine |
| BR | Brazil | IL | Israel | MR | Mauritania | UG | Uganda |
| BY | Belarus | IS | Iceland | MW | Malawi | US | United States of America |
| CA | Canada | IT | Italy | MX | Mexico | UZ | Uzbekistan |
| CF | Central African Republic | JP | Japan | NE | Niger | VN | Viet Nam |
| CG | Congo | KE | Kenya | NL | Netherlands | YU | Yugoslavia |
| CH | Switzerland | KG | Kyrgyzstan | NO | Norway | ZW | Zimbabwe |
| CI | Côte d'Ivoire | KP | Democratic People's Republic of Korea | NZ | New Zealand | | |
| CM | Cameroon | | | PL | Poland | | |
| CN | China | KR | Republic of Korea | PT | Portugal | | |
| CU | Cuba | KZ | Kazakstan | RO | Romania | | |
| CZ | Czech Republic | LC | Saint Lucia | RU | Russian Federation | | |
| DE | Germany | LI | Liechtenstein | SD | Sudan | | |
| DK | Denmark | LK | Sri Lanka | SE | Sweden | | |
| EE | Estonia | LR | Liberia | SG | Singapore | | |

# HLA BINDING PEPTIDES AND THEIR USES

## BACKGROUND OF THE INVENTION

The present invention relates to compositions and methods for preventing, treating or diagnosing a number of pathological states such as viral diseases and cancers. In particular, it provides novel peptides capable of binding selected major histocompatibility complex (MHC) molecules and inducing an immune response.

MHC molecules are classified as either Class I or Class II molecules. Class II MHC molecules are expressed primarily on cells involved in initiating and sustaining immune responses, such as T lymphocytes, B lymphocytes, macrophages, etc. Class II MHC molecules are recognized by helper T lymphocytes and induce proliferation of helper T lymphocytes and amplification of the immune response to the particular immunogenic peptide that is displayed. Class I MHC molecules are expressed on almost all nucleated cells and are recognized by cytotoxic T lymphocytes (CTLs), which then destroy the antigen-bearing cells. CTLs are particularly important in tumor rejection and in fighting viral infections.

The CTL recognizes the antigen in the form of a peptide fragment bound to the MHC class I molecules rather than the intact foreign antigen itself. The antigen must normally be endogenously synthesized by the cell, and a portion of the protein antigen is degraded into small peptide fragments in the cytoplasm. Some of these small peptides translocate into a pre-Golgi compartment and interact with class I heavy chains to facilitate proper folding and association with the subunit β2 microglobulin. The peptide-MHC class I complex is then routed to the cell surface for expression and potential recognition by specific CTLs.

Investigations of the crystal structure of the human MHC class I molecule, HLA-A2.1, indicate that a peptide binding groove is created by the folding of the α1 and α2 domains of the class I heavy chain (Bjorkman et al., Nature 329:506 ( 1987). In these investigations, however, the identity of peptides bound to the groove was not determined.

Buus et al., Science 242:1065 (1988) first described a method for acid elution of bound peptides from MHC. Subsequently, Rammensee and his coworkers (Falk

et al., Nature 351:290 (1991) have developed an approach to characterize naturally processed peptides bound to class I molecules. Other investigators have successfully achieved direct amino acid sequencing of the more abundant peptides in various HPLC fractions by conventional automated sequencing of peptides eluted from class I molecules of the B type (Jardetzky, et al., Nature 353:326 (1991) and of the A2.1 type by mass spectrometry (Hunt, et al., Science 225:1261 (1992). A review of the characterization of naturally processed peptides in MHC Class I has been presented by Rötzschke and Falk (Rötzschke and Falk, Immunol. Today 12:447 (1991).

Sette et al., Proc. Natl. Acad. Sci. USA 86:3296 (1989) showed that MHC allele specific motifs could be used to predict MHC binding capacity. Schaeffer et al., Proc. Natl. Acad. Sci. USA 86:4649 (1989) showed that MHC binding was related to immunogenicity. Several authors (De Bruijn et al., Eur. J. Immunol., 21:2963-2970 (1991); Pamer et al., 991 Nature 353:852-955 (1991)) have provided preliminary evidence that class I binding motifs can be applied to the identification of potential immunogenic peptides in animal models. Class I motifs specific for a number of human alleles of a given class I isotype have yet to be described. It is desirable that the combined frequencies of these different alleles should be high enough to cover a large fraction or perhaps the majority of the human outbred population.

Despite the developments in the art, the prior art has yet to provide a useful human peptide-based vaccine or therapeutic agent based on this work. The present invention provides these and other advantages.

## SUMMARY OF THE INVENTION

The present invention provides compositions comprising immunogenic peptides having binding motifs for HLA molecules. The immunogenic peptides, which bind to the appropriate MHC allele, comprise conserved residues at certain positions which allow the peptides to bind desired HLA molecules.

Epitopes on a number of immunogenic target proteins can be identified using the peptides of the invention. Examples of suitable antigens include prostate cancer specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, human immunodeficiency type-1 virus (HIV1), Kaposi's sarcoma herpes virus (KSHV), human papilloma virus (HPV) antigens, Lassa

virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu. The peptides are thus useful in pharmaceutical compositions for both therapeutic and diagnostic applications.

In particular, the invention provides compositions comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14. Also provided are peptides comprising a conservative substitution of a residue in a peptide shown in Table 3-14. The immunogenic peptide of the invention can be further linked to a second oligopeptide. In some embodiments, the second oligopeptide is a peptide that induces a helper T response.

The invention further provides nucleic acid molecules encoding immunogenic peptides as shown in Tables 3-14, or peptides comprising a conservative substitution of a residue of a peptide shown in Table 3-14. The nucleic acid may further comprise a sequence encoding a second immunogenic peptide or peptide that induces a helper T response.

The peptides provided here can be used to induce a cytotoxic T cell response either *in vivo* or *in vitro*. The methods comprise contacting a cytotoxic T cell with a peptide of the invention.

## Definitions

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of adjacent amino acids. The oligopeptides of the invention are less than about 15 residues in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues.

An "immunogenic peptide" is a peptide which comprises an allele-specific motif such that the peptide will bind an MHC molecule and induce a CTL response. Immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and inducing a cytotoxic T cell response against the antigen from which the immunogenic peptide is derived.

Immunogenic peptides are conveniently identified using the algorithms of the invention. The algorithms are mathematical procedures that produce a score which

enables the selection of immunogenic peptides. Typically one uses the algorithmic score with a "binding threshold" to enable selection of peptides that have a high probability of binding at a certain affinity and will in turn be immunogenic. The algorithm is based upon either the effects on MHC binding of a particular amino acid at a particular position of a peptide or the effects on binding of a particular substitution in a motif containing peptide.

A "conserved residue" is an amino acid which occurs in a significantly higher frequency than would be expected by random distribution at a particular position in a peptide. Typically a conserved residue is one where the MHC structure may provide a contact point with the immunogenic peptide. At least one to three or more, preferably two, conserved residues within a peptide of defined length defines a motif for an immunogenic peptide. These residues are typically in close contact with the peptide binding groove, with their side chains buried in specific pockets of the groove itself. Typically, an immunogenic peptide will comprise up to three conserved residues, more usually two conserved residues.

As used herein, "negative binding residues" are amino acids which if present at certain positions will result in a peptide being a nonbinder or poor binder and in turn fail to be immunogenic i.e. induce a CTL response.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually about 8 to about 11 amino acids, which is recognized by a particular MHC allele. The peptide motifs are typically different for each human MHC allele and differ in the pattern of the highly conserved residues and negative residues.

The binding motif for an allele can be defined with increasing degrees of precision. In one case, all of the conserved residues are present in the correct positions in a peptide and there are no negative residues in positions 1,3 and/or 7.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany it as found in its native state. Thus, the peptides of this invention do not contain materials normally associated with their in situ environment, e.g., MHC I molecules on antigen presenting cells. Even where a protein has been isolated to a homogenous or dominant band, there are trace contaminants in the range of 5-10% of native protein which co-purify with the desired protein. Isolated peptides of this invention do not contain such endogenous co-purified protein.

The term "residue" refers to an amino acid or amino acid mimetic incorporated in an oligopeptide by an amide bond or amide bond mimetic.

## DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention relates to the determination of allele-specific peptide motifs for human Class I MHC (sometimes referred to as HLA) allele subtypes, in particular, peptide motifs recognized by HLA alleles.

For HLA-A2.1 alleles a peptide of 9 amino acids preferrably has the following motif: a first conserved residue at the second position from the N-terminus selected from the group consisting of I, V, A and T and a second conserved residue at the C-terminal position selected from the group consisting of V, L, I, A and M. An alternate motif is one in which the first conserved residue at the second position from the N-terminus selected is from the group consisting of L, M, I, V, A and T and the second conserved residue at the C-terminal position selected from the group consisting of A and M. The amino acid at position 1 is preferrably not an amino acid selected from the group consisting of D, and P. The amino acid at position 3 from the N-terminus is not an amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position 6 from the N-terminus is not an amino acid selected from the group consisting of R, K and H. The amino acid at at position 7 from the N-terminus is not an amino acid selected from the group consisting of R, K, H, D and E.

The HLA-A2.1 binding motif for peptide of 10 residues is as follows: a first conserved residue at the second position from the N-terminus selected from the group consisting of L, M, I, V, A, and T, and a second conserved residue at the C-terminal position selected from the group consisting of V, I, L, A and M. The first and second conserved residues are separated by 7 residues. Preferrably, the amino acid at position 1 is not an amino acid selected from the group consisting of D, E and P. The N-terminal residue is not an amino acid selected from the group consisting of D and E. The residue at position 4 from the N-terminus is not an amino acid selected from the group consisting of A, K, R and H. The amino acid at positon 5 from the N-terminus is not P. The amino acid at position 7 from the N-terminus is not an amino acid selected from the group consisting of R, K and H. The amino acid at position 8 from the N-terminus is not amino acid selected from the group consisting of D, E, R, K and H. The amino acid at position

9 from the N-terminus is not an amino acid selected from the group consisting of R, K and H.

Te motif for HLA-A3.2 comprises from the N-terminus to C-terminus a first conserved residue of L, M, I, V, S, A, T and F at position 2 and a second conserved residue of K, R or Y at the C-terminal end. Other first conserved residues are C, G or D and alternatively E. Other second conserved residues are H or F. The first and second conserved residues are preferably separated by 6 to 7 residues.

The motif for HLA-A1 comprises from the N-terminus to the C-terminus a first conserved residue of T, S or M, a second conserved residue of D or E, and a third conserved residue of Y. Other second conserved residues are A, S or T. The first and second conserved residues are adjacent and are preferably separated from the third conserved residue by 6 to 7 residues. A second motif consists of a first conserved residue of E or D and a second conserved residue of Y where the first and second conserved residues are separated by 5 to 6 residues.

The motif for HLA-A11 comprises from the N-terminus to the C-terminus a first conserved residue of T, V, M, L, I, S, A, G, N, C D, or F at position 2 and a C-terminal conserved residue of K, R, Y or H. The first and second conserved residues are preferably separated by 6 or 7 residues.

The motif for HLA-A24.1 comprises from the N-terminus to the C-terminus a first conserved residue of Y, F or W at position 2 and a C terminal conserved residue of F, I, W, M or L. The first and second conserved residues are preferably separated by 6 to 7 residues.

These motifs are then used to define T cell epitopes from any desired antigen, particularly those associated with human viral diseases, cancers or autoiummune diseases, for which the amino acid sequence of the potential antigen or autoantigen targets is known.

Epitopes on a number of potential target proteins can be identified in this manner. Examples of suitable antigens include prostate specific antigen (PSA), hepatitis B core and surface antigens (HBVc, HBVs) hepatitis C antigens, Epstein-Barr virus antigens, melanoma antigens (e.g., MAGE-1), human immunodeficiency virus (HIV) antigens, human papilloma virus (HPV) antigens, Lassa virus, mycobacterium tuberculosis (MT), p53, CEA, trypanosome surface antigen (TSA) and Her2/neu.

Peptides comprising the epitopes from these antigens are synthesized and then tested for their ability to bind to the appropriate MHC molecules in assays using, for example, purified class I molecules and radioiodonated peptides and/or cells expressing empty class I molecules by, for instance, immunofluorescent staining and flow microfluorometry, peptide-dependent class I assembly assays, and inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary in vitro or in vivo CTL responses that can give rise to CTL populations capable of reacting with virally infected target cells or tumor cells as potential therapeutic agents.

The MHC class I antigens are encoded by the HLA-A, B, and C loci. HLA-A and B antigens are expressed at the cell surface at approximately equal densities, whereas the expression of HLA-C is significantly lower (perhaps as much as 10-fold lower). Each of these loci have a number of alleles. The peptide binding motifs of the invention are relatively specific for each allelic subtype.

For peptide-based vaccines, the peptides of the present invention preferably comprise a motif recognized by an MHC I molecule having a wide distribution in the human population. Since the MHC alleles occur at different frequencies within different ethnic groups and races, the choice of target MHC allele may depend upon the target population. Table 1 shows the frequency of various alleles at the HLA-A locus products among different races. For instance, the majority of the Caucasoid population can be covered by peptides which bind to four HLA-A allele subtypes, specifically HLA-A2.1, A1, A3.2, and A24.1. Similarly, the majority of the Asian population is encompassed with the addition of peptides binding to a fifth allele HLA-A11.2.

TABLE 1

| A Allele/Subtype | N(69)* | A(54) | C(502) |
|---|---|---|---|
| A1 | 10.1(7) | 1.8(1) | 27.4(138) |
| A2.1 | 11.5(8) | 37.0(20) | 39.8(199) |
| A2.2 | 10.1(7) | 0 | 3.3(17) |
| A2.3 | 1.4(1) | 5.5(3) | 0.8(4) |
| A2.4 | - | - | - |
| A2.5 | - | - | - |
| A3.1 | 1.4(1) | 0 | 0.2(0) |
| A3.2 | 5.7(4) | 5.5(3) | 21.5(108) |
| A11.1 | 0 | 5.5(3) | 0 |
| A11.2 | 5.7(4) | 31.4(17) | 8.7(44) |
| A11.3 | 0 | 3.7(2) | 0 |
| A23 | 4.3(3) | - | 3.9(20) |
| A24 | 2.9(2) | 27.7(15) | 15.3(77) |
| A24.2 | - | - | - |
| A24.3 | - | - | - |
| A25 | 1.4(1) | - | 6.9(35) |
| A26.1 | 4.3(3) | 9.2(5) | 5.9(30) |
| A26.2 | 7.2(5) | - | 1.0(5) |
| A26V | - | 3.7(2) | - |
| A28.1 | 10.1(7) | - | 1.6(8) |
| A28.2 | 1.4(1) | - | 7.5(38) |
| A29.1 | 1.4(1) | - | 1.4(7) |
| A29.2 | 10.1(7) | 1.8(1) | 5.3(27) |
| A30.1 | 8.6(6) | - | 4.9(25) |
| A30.2 | 1.4(1) | - | 0.2(1) |
| A30.3 | 7.2(5) | - | 3.9(20) |
| A31 | 4.3(3) | 7.4(4) | 6.9(35) |
| A32 | 2.8(2) | - | 7.1(36) |
| Aw33.1 | 8.6(6) | - | 2.5(13) |
| Aw33.2 | 2.8(2) | 16.6(9) | 1.2(6) |
| Aw34.1 | 1.4(1) | - | - |
| Aw34.2 | 14.5(10) | - | 0.8(4) |
| Aw36 | 5.9(4) | - | - |

Table compiled from B. DuPont, Immunobiology of HLA, Vol. I, Histocompatibility Testing 1987, Springer-Verlag, New York 1989.

* N - negroid; A = Asian; C = caucasoid. Numbers in parenthesis represent the number of individuals included in the analysis.

The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus)

and the carboxyl group to the right (the C-terminus) of each amino acid residue. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G.

The procedures used to identify peptides of the present invention generally follow the methods disclosed in Falk et al., Nature 351:290 (1991), which is incorporated herein by reference. Briefly, the methods involve large-scale isolation of MHC class I molecules, typically by immunoprecipitation or affinity chromatography, from the appropriate cell or cell line. Examples of other methods for isolation of the desired MHC molecule equally well known to the artisan include ion exchange chromatography, lectin chromatography, size exclusion, high performance ligand chromatography, and a combination of all of the above techniques.

In the typical case, immunoprecipitation is used to isolate the desired allele. A number of protocols can be used, depending upon the specificity of the antibodies used. For example, allele-specific mAb reagents can be used for the affinity purification of the HLA-A, HLA-$B_1$, and HLA-C molecules. Several mAb reagents for the isolation of HLA-A molecules are available. The monoclonal BB7.2 is suitable for isolating HLA-A2 molecules. Affinity columns prepared with these mAbs using standard techniques are successfully used to purify the respective HLA-A allele products.

In addition to allele-specific mAbs, broadly reactive anti-HLA-A, B, C mAbs, such as W6/32 and B9.12.1, and one anti-HLA-B, C mAb, B1.23.2, could be used in alternative affinity purification protocols as described in previous applications.

The peptides bound to the peptide binding groove of the isolated MHC molecules are eluted typically using acid treatment. Peptides can also be dissociated from class I molecules by a variety of standard denaturing means, such as heat, pH, detergents, salts, chaotropic agents, or a combination thereof.

Peptide fractions are further separated from the MHC molecules by reversed-phase high performance liquid chromatography (HPLC) and sequenced. Peptides can be separated by a variety of other standard means well known to the artisan, including filtration, ultrafiltration, electrophoresis, size chromatography, precipitation with specific antibodies, ion exchange chromatography, isoelectrofocusing, and the like.

Sequencing of the isolated peptides can be performed according to standard techniques such as Edman degradation (Hunkapiller, M.W., et al., Methods Enzymol. 91, 399 [1983]). Other methods suitable for sequencing include mass spectrometry sequencing of individual peptides as previously described (Hunt, et al., Science 225:1261 (1992), which is incorporated herein by reference). Amino acid sequencing of bulk heterogenous peptides (e.g., pooled HPLC fractions) from different class I molecules typically reveals a characteristic sequence motif for each class I allele.

Definition of motifs specific for different class I alleles allows the identification of potential peptide epitopes from an antigenic protein whose amino acid sequence is known. Typically, identification of potential peptide epitopes is initially carried out using a computer to scan the amino acid sequence of a desired antigen for the presence of motifs. The epitopic sequences are then synthesized. The capacity to bind MHC Class molecules is measured in a variety of different ways. One means is a Class I molecule binding assay as described in the related applications, noted above. Other alternatives described in the literature include inhibition of antigen presentation (Sette, et al., J. Immunol. 141:3893 (1991), in vitro assembly assays (Townsend, et al., Cell 62:285 (1990), and FACS based assays using mutated ells, such as RMA.S (Melief, et al., Eur. J. Immunol. 21:2963 (1991)).

Next, peptides that test positive in the MHC class I binding assay are assayed for the ability of the peptides to induce specific CTL responses in vitro. For instance, Antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells (Inaba, et al., J. Exp. Med. 166:182 (1987); Boog, Eur. J. Immunol. 18:219 [1988]).

Alternatively, mutant mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides, such as the mouse cell lines RMA-S (Kärre, et al.. Nature, 319:675 (1986); Ljunggren, et al., Eur. J. Immunol.

21:2963-2970 (1991)), and the human somatic T cell hybrid, T-2 (Cerundolo, et al., Nature 345:449-452 (1990)) and which have been transfected with the appropriate human class I genes are conveniently used, when peptide is added to them, to test for the capacity of the peptide to induce in vitro primary CTL responses. Other eukaryotic cell lines which could be used include various insect cell lines such as mosquito larvae (ATCC cell lines CCL 125, 126, 1660, 1591, 6585, 6586), silkworm (ATTC CRL 8851), armyworm (ATCC CRL 1711), moth (ATCC CCL 80) and Drosophila cell lines such as a Schneider cell line (see Schneider J. Embryol. Exp. Morphol. 27:353-365 [1927]).

Peripheral blood lymphocytes are conveniently isolated following simple venipuncture or leukapheresis of normal donors or patients and used as the responder cell sources of CTL precursors. In one embodiment, the appropriate antigen-presenting cells are incubated with 10-100 $\mu$M of peptide in serum-free media for 4 hours under appropriate culture conditions. The peptide-loaded antigen-presenting cells are then incubated with the responder cell populations in vitro for 7 to 10 days under optimized culture conditions. Positive CTL activation can be determined by assaying the cultures for the presence of CTLs that kill radiolabeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed form of the relevant virus or tumor antigen from which the peptide sequence was derived.

Specificity and MHC restriction of the CTL is determined by testing against different peptide target cells expressing appropriate or inappropriate human MHC class I. The peptides that test positive in the MHC binding assays and give rise to specific CTL responses are referred to herein as immunogenic peptides.

The immunogenic peptides can be prepared synthetically, or by recombinant DNA technology or from natural sources such as whole viruses or tumors. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides can be synthetically conjugated to native fragments or particles.

The polypeptides or peptides can be a variety of lengths, either in their neutral (uncharged) forms or in forms which are salts, and either free of modifications such as glycosylation, side chain oxidation, or phosphorylation or containing these modifications, subject to the condition that the modification not destroy the biological activity of the polypeptides as herein described.

Desirably, the peptide will be as small as possible while still maintaining substantially all of the biological activity of the large peptide. When possible, it may be desirable to optimize peptides of the invention to a length of 9 or 10 amino acid residues, commensurate in size with endogenously processed viral peptides or tumor cell peptides that are bound to MHC class I molecules on the cell surface.

Peptides having the desired activity may be modified as necessary to provide certain desired attributes, e.g., improved pharmacological characteristics, while increasing or at least retaining substantially all of the biological activity of the unmodified peptide to bind the desired MHC molecule and activate the appropriate T cell. For instance, the peptides may be subject to various changes, such as substitutions, either conservative or non-conservative, where such changes might provide for certain advantages in their use, such as improved MHC binding. By conservative substitutions is meant replacing an amino acid residue with another which is biologically and/or chemically similar, e.g., one hydrophobic residue for another, or one polar residue for another. The substitutions include combinations such as Gly, Ala; Val, Ile, Leu, Met; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. The effect of single amino acid substitutions may also be probed using D-amino acids. Such modifications may be made using well known peptide synthesis procedures, as described in e.g., Merrifield, Science 232:341-347 (1986), Barany and Merrifield, The Peptides, Gross and Meienhofer, eds. (N.Y., Academic Press), pp. 1-284 (1979); and Stewart and Young, Solid Phase Peptide Synthesis, (Rockford, Ill., Pierce), 2d Ed. (1984), incorporated by reference herein.

The peptides can also be modified by extending or decreasing the compound's amino acid sequence, e.g., by the addition or deletion of amino acids. The peptides or analogs of the invention can also be modified by altering the order or composition of certain residues, it being readily appreciated that certain amino acid residues essential for biological activity, e.g., those at critical contact sites or conserved residues, may generally not be altered without an adverse effect on biological activity. The non-critical amino acids need not be limited to those naturally occurring in proteins, such as L-α-amino acids, or their D-isomers, but may include non-natural amino acids as well, such as β-γ-δ-amino acids, as well as many derivatives of L-α-amino acids.

Typically, a series of peptides with single amino acid substitutions are employed to determine the effect of electrostatic charge, hydrophobicity, etc. on binding.

For instance, a series of positively charged (e.g., Lys or Arg) or negatively charged (e.g., Glu) amino acid substitutions are made along the length of the peptide revealing different patterns of sensitivity towards various MHC molecules and T cell receptors. In addition, multiple substitutions using small, relatively neutral moieties such as Ala, Gly, Pro, or similar residues may be employed. The substitutions may be homo-oligomers or hetero-oligomers. The number and types of residues which are substituted or added depend on the spacing necessary between essential contact points and certain functional attributes which are sought (e.g., hydrophobicity versus hydrophilicity). Increased binding affinity for an MHC molecule or T cell receptor may also be achieved by such substitutions, compared to the affinity of the parent peptide. In any event, such substitutions should employ amino acid residues or other molecular fragments chosen to avoid, for example, steric and charge interference which might disrupt binding.

Amino acid substitutions are typically of single residues. Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a final peptide. Substitutional variants are those in which at least one residue of a peptide has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the following Table 2 when it is desired to finely modulate the characteristics of the peptide.

TABLE 2

| Original Residue | Exemplary Substitution |
|---|---|
| Ala | Ser |
| Arg | Lys, His |
| Asn | Gln |
| Asp | Glu |
| Cys | Ser |
| Gln | Asn |
| Glu | Asp |
| Gly | Pro |
| His | Lys; Arg |
| Ile | Leu; Val |
| Leu | Ile; Val |
| Lys | Arg; His |
| Met | Leu; Ile |
| Phe | Tyr; Trp |
| Ser | Thr |
| Thr | Ser |
| Trp | Tyr; Phe |
| Tyr | Trp; Phe |
| Val | Ile; Leu |
| Pro | Gly |

Substantial changes in function (e.g., affinity for MHC molecules or T cell receptors) are made by selecting substitutions that are less conservative than those in Table 2, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in peptide properties will be those in which (a) hydrophilic residue, e.g. seryl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a residue having an electropositive side chain, e.g., lysl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (c) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

The peptides may also comprise isosteres of two or more residues in the immunogenic peptide. An isostere as defined here is a sequence of two or more residues that can be substituted for a second sequence because the steric conformation of the first sequence fits a binding site specific for the second sequence. The term specifically includes peptide backbone modifications well known to those skilled in the art. Such modifications include modifications of the amide nitrogen, the α-carbon, amide carbonyl, complete replacement of the amide bond, extensions, deletions or backbone crosslinks. See, generally, Spatola, Chemistry and Biochemistry of Amino Acids, peptides and Proteins, Vol. VII (Weinstein ed., 1983).

Modifications of peptides with various amino acid mimetics or unnatural amino acids are particularly useful in increasing the stability of the peptide in vivo. Stability can be assayed in a number of ways. For instance, peptidases and various biological media, such as human plasma and serum, have been used to test stability. See, e.g., Verhoef et al., Eur. J. Drug Metab. Pharmacokin. 11:291-302 (1986). Half life of the peptides of the present invention is conveniently determined using a 25% human serum (v/v) assay. The protocol is generally as follows. Pooled human serum (Type AB, non-heat inactivated) is delipidated by centrifugation before use. The serum is then diluted to 25% with RPMI tissue culture media and used to test peptide stability. At predetermined time intervals a small amount of reaction solution is removed and added to either 6% aqueous trichloracetic acid or ethanol. The cloudy reaction sample is cooled

(4°C) for 15 minutes and then spun to pellet the precipitated serum proteins. The presence of the peptides is then determined by reversed-phase HPLC using stability-specific chromatography conditions.

The peptides of the present invention or analogs thereof which have CTL stimulating activity may be modified to provide desired attributes other than improved serum half life. For instance, the ability of the peptides to induce CTL activity can be enhanced by linkage to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. Particularly preferred immunogenic peptides/T helper conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, e.g., Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues. Alternatively, the CTL peptide may be linked to the T helper peptide without a spacer.

The immunogenic peptide may be linked to the T helper peptide either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated. Exemplary T helper peptides include tetanus toxoid 830-843, influenza 307-319, malaria circumsporozoite 382-398 and 378-389.

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes CTL. Lipids have been identified as agents capable of priming CTL in vivo against viral antigens. For example, palmitic acid residues can be attached to the alpha and epsilon amino groups of a Lys residue and then linked, e.g., via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be injected directly in a micellar form, incorporated into a liposome or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. In a preferred embodiment a particularly effective immunogen comprises palmitic acid attached to alpha and epsilon amino groups

of Lys, which is attached via linkage, e.g., Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, E. coli lipoproteins, such as tripalmitoyl-S-glycerylcysteinlyseryl-serine ($P_3CSS$) can be used to prime virus specific CTL when covalently attached to an appropriate peptide. See, Deres et al., Nature 342:561-564 (1989), incorporated herein by reference. Peptides of the invention can be coupled to $P_3CSS$, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Further, as the induction of neutralizing antibodies can also be primed with $P_3CSS$ conjugated to a peptide which displays an appropriate epitope, the two compositions can be combined to more effectively elicit both humoral and cell-mediated responses to infection.

In addition, additional amino acids can be added to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support, or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide. Modification at the C terminus in some cases may alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-$NH_2$ acylation, e.g., by alkanoyl ($C_1$-$C_{20}$) or thioglycolyl acetylation, terminal-carboxyl amidation, e.g., ammonia, methylamine, etc. In some instances these modifications may provide sites for linking to a support or other molecule.

The peptides of the invention can be prepared in a wide variety of ways. Because of their relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young, Solid Phase Peptide Synthesis, 2d. ed., Pierce Chemical Co. (1984), supra.

Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art,

as described generally in Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor, New York (1982), which is incorporated herein by reference. Thus, fusion proteins which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

As the coding sequence for peptides of the length contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci et al., J. Am. Chem. Soc. 103:3185 (1981), modification can be made simply by substituting the appropriate base(s) for those encoding the native peptide sequence. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

The peptides of the present invention and pharmaceutical and vaccine compositions thereof are useful for administration to mammals, particularly humans, to treat and/or prevent viral infection and cancer. Examples of diseases which can be treated using the immunogenic peptides of the invention include prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV and condlyloma acuminatum.

For pharmaceutical compositions, the immunogenic peptides of the invention are administered to an individual already suffering from cancer or infected with the virus of interest. Those in the incubation phase or the acute phase of infection can be treated with the immunogenic peptides separately or in conjunction with other treatments, as appropriate. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL response to the virus or tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to

accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial immunization (that is for therapeutic or prophylactic administration) from about 1.0 μg to about 5000 μg of peptide for a 70 kg patient, followed by boosting dosages of from about 1.0 μg to about 1000 μg of peptide pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition by measuring specific CTL activity in the patient's blood. It must be kept in mind that the peptides and compositions of the present invention may generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, in view of the minimization of extraneous substances and the relative nontoxic nature of the peptides, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions.

For therapeutic use, administration should begin at the first sign of viral infection or the detection or surgical removal of tumors or shortly after diagnosis in the case of acute infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In chronic infection, loading doses followed by boosting doses may be required.

Treatment of an infected individual with the compositions of the invention may hasten resolution of the infection in acutely infected individuals. For those individuals susceptible (or predisposed) to developing chronic infection the compositions are particularly useful in methods for preventing the evolution from acute to chronic infection. Where the susceptible individuals are identified prior to or during infection, for instance, as described herein, the composition can be targeted to them, minimizing need for administration to a larger population.

The peptide compositions can also be used for the treatment of chronic infection and to stimulate the immune system to eliminate virus-infected cells in carriers. It is important to provide an amount of immuno-potentiating peptide in a formulation and mode of administration sufficient to effectively stimulate a cytotoxic T cell response. Thus, for treatment of chronic infection, a representative dose is in the range of about 1.0 μg to about 5000 μg, preferably about 5 μg to 1000 μg for a 70 kg patient per dose.

Immunizing doses followed by boosting doses at established intervals, e.g., from one to four weeks, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic infection, administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a period thereafter.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral or local administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

The concentration of CTL stimulatory peptides of the invention in the pharmaceutical formulations can vary widely, i.e., from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected.

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or targeted selectively to infected cells, as well as increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to, e.g., a receptor prevalent among lymphoid cells, such as monoclonal

antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the selected therapeutic/immunogenic peptide compositions. Liposomes for use in the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, e.g., liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, e.g., Szoka et al., Ann. Rev. Biophys. Bioeng. 9:467 (1980), U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369, incorporated herein by reference.

For targeting to the immune cells, a ligand to be incorporated into the liposome can include, e.g., antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight

of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, e.g., lecithin for intranasal delivery.

In another aspect the present invention is directed to vaccines which contain as an active ingredient an immunogenically effective amount of an immunogenic peptide as described herein. The peptide(s) may be introduced into a host, including humans, linked to its own carrier or as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptides are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the virus or tumor cells. Useful carriers are well known in the art, and include, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly(lysine:glutamic acid), influenza, hepatitis B virus core protein, hepatitis B virus recombinant vaccine and the like. The vaccines can also contain a physiologically tolerable (acceptable) diluent such as water, phosphate buffered saline, or saline, and further typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are materials well known in the art. And, as mentioned above, CTL responses can be primed by conjugating peptides of the invention to lipids, such as $P_3CSS$. Upon immunization with a peptide composition as described herein, via injection, aerosol, oral, transdermal or other route, the immune system of the host responds to the vaccine by producing large amounts of CTLs specific for the desired antigen, and the host becomes at least partially immune to later infection, or resistant to developing chronic infection.

Vaccine compositions containing the peptides of the invention are administered to a patient susceptible to or otherwise at risk of viral infection or cancer to elicit an immune response against the antigen and thus enhance the patient's own immune response capabilities. Such an amount is defined to be an "immunogenically effective dose." In this use, the precise amounts again depend on the patient's state of health and weight, the mode of administration, the nature of the formulation, etc., but generally range from about 1.0 $\mu$g to about 5000 $\mu$g per 70 kilogram patient, more commonly from about 10 $\mu$g to about 500 $\mu$g mg per 70 kg of body weight.

In some instances it may be desirable to combine the peptide vaccines of the invention with vaccines which induce neutralizing antibody responses to the virus of interest, particularly to viral envelope antigens.

For therapeutic or immunization purposes, nucleic acids encoding one or more of the peptides of the invention can also be admisitered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nulceic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff *et. al.*, *Science* 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. The nucleci acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in WO 96/18372; WO 93/24640; Mannino and Gould-Fogerite (1988) *BioTechniques* 6(7): 682-691; Rose U.S. Pat No. 5,279,833; WO 91/06309; and Felgner *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84: 7413-7414. The peptides of the invention can also be expressed by attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848, incorporated herein by reference. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover et al. (Nature 351:456-460 (1991)) which is incorporated herein by reference. A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, e.g., Salmonella typhi vectors and the like, will be apparent to those skilled in the art from the description herein.

A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding multiple epitopes of the invention. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding

DNA sequences are directly adjoined, creating a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte epitopes, a leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL epitopes.

The minigene sequence is converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) are synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. he ends of the oligonucleotides are joined using T4 DNA ligase. This synthetic minigene, encoding the CTL epitope polypeptide, can then cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are included in the vector to ensure expression in the target cells. Several vector elements are required: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. *See*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences can also be considered for increasing minigene expression. It has recently been proposed that immunostimulatory sequences (ISSs or CpGs) play a role in the immunogenicity of DNA vaccines. These sequences could be included in the vector, outside the minigene coding sequence, if found to enhance immunogenicity.

In some embodiments, a bicistronic expression vector, to allow production of the minigene-encoded epitopes and a second protein included to enhance or decrease immunogenicity can be used. Examples of proteins or polypeptides that could beneficially

enhance the immune response if co-expressed include cytokines (e.g., IL2, IL12, GM-CSF), cytokine-inducing molecules (e.g. LeIF) or costimulatory molecules. Helper (HTL) epitopes could be joined to intracellular targeting signals and expressed separately from the CTL epitopes. This would allow direction of the HTL epitopes to a cell compartment different than the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the MHC class II pathway, thereby improving CTL induction. In contrast to CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF-β) may be beneficial in certain diseases.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

Therapeutic quantities of plasmid DNA are produced by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate fermentation medium (such as Terrific Broth), and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by Quiagen. If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). A variety of methods have been described, and new techniques may become available. As noted above, nucleic acids are conveniently formulated with cationic lipids. In addition, glycolipids, fusogenic liposomes, peptides and compounds referred to collectively as protective, interactive, non-condensing (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and MHC class I presentation of minigene-encoded CTL epitopes. The plasmid DNA is

introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 labeled and used as target cells for epitope-specific CTL lines. Cytolysis, detected by 51Cr release, indicates production of MHC presentation of minigene-encoded CTL epitopes.

*In vivo* immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human MHC molecules are immunized with the DNA product. The dose and route of administration are formulation dependent (e.g. IM for DNA in PBS, IP for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for 1 week in the presence of peptides encoding each epitope being tested. These effector cells (CTLs) are assayed for cytolysis of peptide-loaded, chromium-51 labeled target cells using standard techniques. Lysis of target cells sensitized by MHC loading of peptides corresponding to minigene-encoded epitopes demonstrates DNA vaccine function for *in vivo* induction of CTLs.

Antigenic peptides may be used to elicit CTL ex vivo, as well. The resulting CTL, can be used to treat chronic infections (viral or bacterial) or tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a peptide vaccine approach of therapy. Ex vivo CTL responses to a particular pathogen (infectious agent or tumor antigen) are induced by incubating in tissue culture the patient's CTL precursor cells (CTLp) together with a source of antigen-presenting cells (APC) and the appropriate immunogenic peptide. After an appropriate incubation time (typically 1-4 weeks), in which the CTLp are activated and mature and expand into effector CTL, the cells are infused back into the patient, where they will destroy their specific target cell (an infected cell or a tumor cell).

The peptides may also find use as diagnostic reagents. For example, a peptide of the invention may be used to determine the susceptibility of a particular individual to a treatment regimen which employs the peptide or related peptides, and thus may be helpful in modifying an existing treatment protocol or in determining a prognosis for an affected

individual. In addition, the peptides may also be used to predict which individuals will be at substantial risk for developing chronic infection.

The following example is offered by way of illustration, not by way of limitation.

Example 1

Class I antigen isolation was carried out as described in the related applications, noted above. Naturally processed peptides were then isolated and sequenced as described there. An allele-specific motif and algorithms were determined and quantitative binding assays were carried out.

Using the motifs identified above for various HLA alleles, amino acid sequences from a number of antigens were analyzed for the presence of these motifs. Tables 3- ** provide the results of these searches.

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference.

Table 3

| Sequence | Antigen | Molecule |
|---|---|---|
| FTFSPTYKAFLSK | HBV | POL |
| GTLPQEHIVLKLK | HBV | POL |
| FTFSPTYKAFLCK | HBV | POL |
| GTLPQEHIVLKIK | HBV | POL |
| LVVSYVNTNMGLK | HBV | POL |
| STTDLEAYFKDCLFK | HBV | X |
| LVVSYVNVNMGLK | HBV | NUC |
| GTLPQDHIVQKIK | HBV | POL |
| STSSCLHQSAVRK | HBV | POL |
| TTVNAHQILPKVLHK | HBV | X |
| RTPARVTGGVFLVDK | HBV | POL |

| Sequence | Antigen | Molecule |
|---|---|---|
| HTTNFASK | HBV ayw | |
| FTFSPTYK | HBV ayw | |
| PTYKAFLCKQY | HBVayw | |
| CTTPAQGTSMY | HBVayw | |
| PTSCPPTCPGY | HBVayw | |
| FSQFSRGNY | HBVayw | |
| LMPLYACIQSK | HBVayw | |
| RVTGGVFLVDK | HBVayw | POL |
| HTLWKAGILYK | HBVayw | |
| QTRHYLHTLWK | HBVayw | |
| GTDNSVVLSRK | HBVayw | |
| SYVNTNMGLKF | HBVayw | |
| LYSILSPF | HBVayw | |
| WYWGPSLYSIL | HBVayw | |
| LYSILSPFLPL | HBVayw | |
| PYKEFGATVEL | HBVayw | |
| CTWMNSTGFTK | HCV | |
| MYVGDLCGSVF | HCV | |
| VYLLPRRGPRL | HCV | |
| ITKIQNFRVYY | HIV | |
| KVYLAWVPAHK | HIV | |
| KMIGGIGGFIK | HIV | |
| IVASCDKCQLK | HIV | |
| KVKQWPLTEEK | HIV | |
| TVNDIQKLVGK | HIV | |
| DVKQLTEAVQK | HIV | |
| AVVIQDNSDIK | HIV | |
| WTYQIYQEPFK | HIV | |
| VTVYYGVPVWK | HIV | |
| LTEDRWNKPQK | HIV | |
| ATDIQTKELQK | HIV | |
| QTKELQKQITK | HIV | |

| Sequence | Antigen | Molecule |
|---|---|---|
| WTVQPIVLPEK | HIV | |
| QVPLRPMTYK | HIV nef 73-82 | |
| QVPLYPMTFK | HIV nef 73-82 | |
| VPLRPMTYK | HIV nef 74-82 | |
| AVDLYHFLK | HIV nef 84-94 | |
| AVDLSHFLK | HIV nef 84-94 | |
| ATLYCVHQR | HIV, p17, 82-90 | |
| RLRDLLLIV | HIV-1 NL43 768-776 | |
| RLRDLLLIVTR | HIV-1 NL43 768-778 | |
| RLRDYLLIVTR | HIV-1 NL43 768-778 | |
| LRDLLLIVTR | HIV-1 NL43 769-778 | |
| QIYQEPFKNLK | HIV-1 RT 507-517 | |
| AVFIHNFK | HIVcon | |
| RTLNAWVK | HIVcon | |
| ETAYFlLK | HIVcon | |
| RLRPGGKKK | HIVgag p17/2 | |
| KIRLRPGGKK | HIVgag p17/2 | |
| KIRLRPGGK | HIVgag p17/2 | |
| ETTDLYCY | HPV16 | E7 |
| GTLGIVCPICSQK | HPV16 | E7 |

| Sequence | Antigen | Molecule |
|---|---|---|
| LMGTLGIVCPICSQK | HPV16 | E7 |
| AVCDKCLK | HPV16 | E6 |
| PYAVCDKCLKF | HPV16 | E6 |
| HYCYSLYGTTL | HPV16 | E6 |
| FYSRIREL | HPV16 | E6 |
| TLEKLTNTGLY | HPV18 | E6 |
| KTVLELTEVFEFAFK | HPV18 | E6 |
| TMLCMCCK | HPV18 | E7 |
| NTSLQDIEITCVYCK | HPV18 | E6 |
| EVFEFAFK | HPV18 | E6 |
| KQSSKALQR | Leukemia | b3A2 CMI |
| ATGFKQSSK | Leukemia | b3A2 CMI |
| HSATGFKQSSK | Leukemia | b3A2 CMI |
| FKQSSKALQR | Leukemia | b3A2 CMI |
| VTCLGLSY | MAGE1 | |
| ITKKVADLVGFLLLK | MAGE1 | |
| LVGFLLLK | MAGE1 | |
| VTKAEMLESVIKNYK | MAGE1 | |
| TSCILESLFR | MAGE1 | |
| NYKHCFPEI | MAGE1 | |
| SYVLVTCL | MAGE1 | |
| ETDPISHTY | MAGE1(a) | |
| ETDPTSHLY | MAGE1(a) | |
| ETDPTSNTY | MAGE1(a) | |
| ETDPTSHVY | MAGE1(a) | |
| ETDPTSHSY | MAGE1(a) | |
| ETDPASHTY | MAGE1(a) | |
| EVDPTSHTY | MAGE1(a) | |
| ETDPTGHTY | MAGE1(a) | |
| ETDRTSHTY | MAGE1(a) | |
| EADPTSHTY | MAGE1(a) | |
| ETVPTSHTY | MAGE1(a) | |

| Sequence | Antigen | Molecule |
|---|---|---|
| ETDPTSHTY | MAGE1 consensus | |
| ETDPTGHSY | MAGE1 T(a) | |
| MFPDLESEF | MAGE2 | |
| TTINYTLWR | MAGE2 | |
| VIFSKASEY | MAGE2 | |
| LVHFLLLKY | MAGE2 | |
| LVHFLLLKY | MAGE2 | |
| LVHFLLLKYR | MAGE2 | |
| PVIFSKASEY | MAGE2 | |
| STTINYTLWR | MAGE2 | |
| VVEVVPISH | MAGE2 | |
| EYLQLVFGI | MAGE2 | |
| IFSKASEYL | MAGE2 | |
| SFSTTINYTL | MAGE2 | |
| LYILVTCLGL | MAGE2 | |
| FATCLGLSY | MAGE3 | |
| VVGNWQYFFPVIFSK | MAGE3 | |
| LIIVLAIIAR | MAGE3 | |
| YFFPVIFSK | MAGE3 | |
| NWQYFFPVI | MAGE3 | |
| NWQYFFPVIF | MAGE3 | |
| IFSKASSSL | MAGE3 | |
| EVDPTSNTY | MAGE41 | |
| RYPLTFGWCY | nef/182 | |
| RYPLTFGWC | nef/182 | |
| ATQIPSYK | PAP | |
| LTELYFEK | PAP | |
| HSFPHPLY | PSA | |
| TQEPALGTTCY | PSA | |
| VTKFMLCAGRWTGGK | PSA | |
| HVISNDVCAQVHPQK | PSA | |

| Sequence | Antigen | Molecule |
|---|---|---|
| LYDMSLLKNRF | PSA | |
| ETDPTGHSY | T2 analog of MAGE-3 | |

Table 4

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0300 | HLDMLRHLY | 9 | c-ERB2 | | | 42 | 1 | 9 1 | | 0.037 | 0.0072 | |
| 1.0346 | LLDIDETEY | 9 | c-ERB2 | | | 869 | 1 | 7 6 | | 0 0013 | 0 | |
| 1.0305 | GTQLFEDNY | 9 | c-ERB2 | | | 1111 | 1 | 0.18 | | 0 | 0.028 | |
| 1.0355 | LTCSPQPEY | 9 | c-ERB2 | | | 1131 | 1 | 0.13 | | 0 | 0.0061 | |
| 1.0317 | ETLEEITGY | 9 | c-ERB2 | | | 401 | 1 | 0.043 | | <0.0002 | <0.0002 | |
| 1.0338 | QLVTQLMPY | 9 | c-ERB2 | | | 795 | 1 | 0.0024 | | 0.011 | 0.0039 | |
| 1.0749 | FTHQSDVWSY | 10 | c-ERB2 | | | 899 | 1 | 2.7 | | 0.0003 | 0.0005 | |
| 1.0747 | RLLDIDETEY | 10 | c-ERB2 | | | 868 | 1 | 1.3 | | 0.0017 | 0 | |
| 1.0715 | TLEEITGYLY | 10 | c-ERB2 | | | 402 | 1 | 1.1 | | 0 | 0 | |
| 1.0737 | YVMAGVGSPY | 10 | c-ERB2 | | | 772 | 1 | 1.1 | 0 | 0.010 | 0.012 | 0 |
| 1.0764 | GTPTAENPEY | 10 | c-ERB2 | | | 1239 | 1 | 0.063 | | <0.0002 | 0.0022 | |
| 1.0724 | RVLQGLPREY | 10 | c-ERB2 | | | 545 | 1 | <0.0015 | | 0.035 | 0.0050 | |
| 1.0705 | LIQRNPQLCY | 10 | c-ERB2 | | | 154 | 1 | 0.030 | | 0.0012 | <0.0002 | |
| 1.0693 | VVQGNLELTY | 10 | c-ERB2 | | | 55 | 1 | 0.018 | | 0.0024 | 0.011 | |
| 1.0756 | MGDLVDAEEY | 10 | c-ERB2 | | | 1014 | 1 | 0.012 | | <0.0002 | <0.0002 | |
| 1.1028 | KIRKYTMRR | 9 | c-ERB2 | | | 681 | 3,11 | | | 0.76 | 0.0018 | |
| 1.1027 | VVPGILIKR | 9 | c-ERB2 | | | 669 | 3,11 | | | 0.11 | 0.72 | |
| 1.0344 | LVKSPNHVK | 9 | c-ERB2 | | | 852 | 3,11 | | | 0.48 | 0.070 | |
| 1.0335 | VLRENTSPK | 9 | c-ERB2 | | | 754 | 3,11 | | | 0.40 | 0.013 | |
| 1.0329 | ILIKRRQQK | 9 | c-ERB2 | | | 673 | 3,11 | | | 0.38 | 0.0097 | |
| 1.0311 | ILWKDIFHK | 9 | c-ERB2 | | | 167 | 3,11 | | | 0.28 | 0.31 | |
| 1.1033 | KITDFGLAR | 9 | c-ERB2 | | | 860 | 3,11 | | | 0.17 | 0.24 | |
| 1.0869 | GVVPGILIK | 9 | c-ERB2 | | | 668 | 3,11 | | | 0.0047 | 0.089 | |
| 1.0299 | QVCTGTDMK | 9 | c-ERB2 | | | 24 | 3,11 | | | 0.0007 | 0.052 | |
| 1.1031 | LLDHVRENR | 9 | c-ERB2 | | | 806 | 3,11 | | | 0.037 | <0.0006 | |
| 1.1026 | CVNCSQFLR | 9 | c-ERB2 | | | 528 | 3,11 | | | 0.0015 | 0.031 | |
| 1.1023 | TVCAGGCAR | 9 | c-ERB2 | | | 218 | 3,11 | | | 0.0004 | 0.023 | |
| 1.0331 | ILKETELRK | 9 | c-ERB2 | | | 714 | 3,11 | | | 0.019 | 0.0023 | |
| 1.1024 | VTAEDGTQR | 9 | c-ERB2 | | | 322 | 3,11 | | | <0.0002 | 0.014 | |
| 1.0326 | DLSYMPIWK | 9 | c-ERB2 | | | 607 | 3,11 | | | 0.0005 | 0.010 | |
| 1.0707 | TILWKDIFHK | 10 | c-ERB2 | | | 166 | 3,11 | | | 0.043 | 3.6 | |
| 1.0712 | GTQRCEKCSK | 10 | c-ERB2 | | | 327 | 3,11 | | | 0.021 | 0.61 | |
| 1.0736 | KVLRENTSPK | 10 | c-ERB2 | | | 753 | 3,11 | | | 0.38 | 0.22 | |
| 1.0702 | QLRSLTEILK | 10 | c-ERB2 | | | 141 | 3,11 | | | 0.20 | 0 013 | |
| 1.1142 | RLVHRDLAAR | 10 | c-ERB2 | | | 840 | 3,11 | | | 0.18 | 0 | |
| 1.0741 | LLNWCMQIAK | 10 | c-ERB2 | | | 822 | 3,11 | | | 0.14 | 0 14 | |
| 1.0752 | TIDVYMIMVK | 10 | c-ERB2 | | | 948 | 3,11 | | | 0.013 | 0.12 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0731 | RILKETELRK | 10 | c-ERB2 | | | 713 | 3,11 | | | 0.057 | 0.11 | |
| 1.0745 | VLVKSPNHVK | 10 | c-ERB2 | | | 851 | 3,11 | | | 0.082 | 0.0072 | |
| 1.1131 | SVFQNLQVIR | 10 | c-ERB2 | | | 423 | 3,11 | | | 0.017 | 0.075 | |
| 1.1133 | FTVPWDQLFR | 10 | c-ERB2 | | | 478 | 3,11 | | | 0.0035 | 0.072 | |
| 1.1127 | ILKGGVLIQR | 10 | c-ERB2 | | | 144 | 3,11 | | | 0.040 | 0.0005 | |
| 1.1143 | LVSEFSRMAR | 10 | c-ERB2 | | | 972 | 3,11 | | | 0.0072 | 0.033 | |
| 1.1136 | GVVFGILIKR | 10 | c-ERB2 | | | 668 | 3,11 | | | 0.018 | 0.033 | |
| 1.0726 | CVARCPSGVK | 10 | c-ERB2 | | | 596 | 3,11 | | | 0.022 | 0.0042 | |
| 1.1137 | VVFGILIKRR | 10 | c-ERB2 | | | 669 | 3,11 | | | 0.0030 | 0.016 | |
| 1.0728 | GILIKRRQQK | 10 | c-ERB2 | | | 672 | 3,11 | | | 0.015 | 0.0014 | |
| 1.1129 | RTVCAGGCAR | 10 | c-ERB2 | | | 217 | 3,11 | | | 0.0068 | 0.013 | |
| 1.1134 | GLACHQLCAR | 10 | c-ERB2 | | | 508 | 3,11 | | | 0.011 | 0 | |
| 1.1139 | KIPVAIKVLR | 10 | c-ERB2 | | | 747 | 3,11 | | | 0.0009 | 0.0099 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0791 | VGEADYFEY | 9 | EBNA1 | | | 419 | 1 | 0.016 | | | | |
| 1.0795 | PLRESIVCY | 9 | EBNA1 | | | 553 | 1 | 0.1110 | | | | |
| 1.0681 | PVGEADYFEY | 10 | EBNA1 | | | 418 | 1 | 0.015 | | | | |
| 1.0683 | GTWVAGVFVY | 10 | EBNA1 | | | 501 | 1 | 0.114 | | | | |
| 1.0293 | GVFVYGGSK | 9 | EBNA1 | | | 506 | 3,11 | | | 0.30 | 0.61 | |
| 1.1016 | KTSLYNLRR | 9 | EBNA1 | | | 514 | 3,11 | | | 0.31 | 0.12 | |
| 1.0297 | AIKDLVMTK | 9 | EBNA1 | | | 578 | 3,11 | | | 0.048 | 0.034 | |
| 1.0687 | QTHIFAEVLK | 10 | EBNA1 | | | 567 | 3,11 | | | 0.010 | 0.21 | |
| 1.1124 | GTALAIPQCR | 10 | EBNA1 | | | 523 | 3,11 | | | 0.0028 | 0.056 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5.0105 | CTELKLSDY | 9 | FLU | A | NP | 44 | 1 | 3.6 | | | | |
| 5.0106 | STLELRSRY | 9 | FLU | A | NP | 377 | 1 | 0.020 | | | | |
| 5.0044 | ILRGSVAHK | 9 | FLU | A | NP | 265 | 3 | | | 1.5 | 0.0037 | |
| 5.0051 | RMCNILKGK | 9 | FLU | A | NP | 221 | 3 | | | 0.27 | 0.062 | |
| 5.0046 | LMQGSTLPR | 9 | FLU | A | NP | 166 | 3 | | | 0.031 | 0.10 | |
| 5.0048 | MIDGKGRFY | 9 | FLU | A | NP | 32 | 3 | | | 0.059 | 0.0010 | |
| 5.0049 | MVLSAFDER | 9 | FLU | A | NP | 66 | 3 | | | 0.0016 | 0.041 | |
| 5.0054 | YTQMCTELK | 9 | FLU | A | NP | 40 | 3 | | | 0.0031 | 0.030 | |
| 5.0042 | GINDRNFWR | 9 | FLU | A | NP | 200 | 3 | | | 0.0028 | 0.024 | |
| 5.0104 | SLMQGSTLPR | 10 | FLU | A | NP | 165 | 3 | | | 0.12 | 0.84 | |
| 5.0095 | KMIDGIGRFY | 10 | FLU | A | NP | 31 | 3 | | | 0.50 | 0.0079 | |
| 5.0096 | LILRGSVAHK | 10 | FLU | A | NP | 264 | 3 | | | 0.36 | 0.037 | |
| 5.0102 | RSGAAGAAVK | 10 | FLU | A | NP | 175 | 3 | | | 0.019 | 0.0046 | |
| 5.0105 | SSTLELRSRY | 10 | FLU | A | NP | 376 | 3 | | | 0.0018 | 0.016 | |
| 5.0103 | RSRYWAIRTR | 10 | FLU | A | NP | 382 | 3 | | | 0.012 | 0 | |
| 5.0101 | RMVLSAFDER | 10 | FLU | A | NP | 65 | 3 | | | 0.0014 | 0.010 | |
| 5.0061 | FYIQMCTEL | 9 | FLU | A | NP | 39 | 24 | | | | | 2.9 |
| 5.0060 | AYEIMQNIL | 9 | FLU | A | NP | 218 | 24 | | | | | 0.031 |
| 5.0112 | RFYIQMCTEL | 10 | FLU | A | NP | 38 | 24 | | | | | 0.15 |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A21 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0155 | LLDTASALY | 9 | HBV | adr | CORE | 420 | 1 | 25 | 0.0007 | 0.0037 | 0 | |
| 1.0186 | SLDVSAAFY | 9 | HBV | adr | POL | 1011 | 1 | 17.2 | | 0.0008 | 0.0006 | |
| 2.0125 | PTTGRTSLY | 9 | HBV | ALL | | 1,382 | 1 | 1.3 | | 0.0008 | 0 | |
| 2.0126 | MSTTDLEAY | 9 | HBV | adr | | 1,521 | 1 | 0.85 | | <0.0008 | 0 | |
| 1.0208 | PTTGRTSLY | 9 | HBV | adr | POL | 1382 | 1 | 0.77 | | 0 | 0 | |
| 1.0387 | LTKQYLNLY | 9 | HBV | adw | POL | 1280 | 1 | 0.50 | | 0.0003 | 0.0075 | |
| 1.0166 | KVGNFTGLY | 9 | HBV | adr | POL | 629 | 1 | 0.068 | | 0.30 | 0.014 | |
| 2.0127 | MSPTDLEAY | 9 | HBV | adw | | 1,550 | 1 | 0.067 | | | | |
| 2.0120 | PSQPSRGNY | 9 | HBV | ayw | | 984 | 1 | 0.057 | | | | |
| 2.0112 | PSSWAFAKY | 9 | HBV | adw | | 316 | 1 | 0.054 | | | | |
| 2.0119 | QSAVRKEAY | 9 | HBV | adw | | 881 | 1 | 0.025 | | | | |
| 1.0174 | PLDKGIKPY | 9 | HBV | adr | POL | 698 | 1 | 0.019 | | <0.0002 | <0.0002 | |
| 1.0078 | SLMLLYKTY | 9 | HBV | adw | POL | 1092 | 1 | 0.017 | | | | |
| 2.0115 | ASRDLVVSY | 9 | HBV | ayw | | 499 | 1 | 0.013 | | | | |
| 2.0124 | PSRGRLGLY | 9 | HBV | adr/adw | | 1,364 | 1 | 0.011 | | | | |
| 2.0121 | SSTSRNTNY | 9 | HBV | adr | | 1,036 | 1 | 0.0097 | | | | |
| 1.0619 | DLLDTASALY | 10 | HBV | adr | CORE | 419 | 1 | 11.1 | | 0 | 0 | |
| 1.0613 | LLDPAVRGLY | 10 | HBV | adr | ENV | 120 | 1 | 6.3 | | 0.17 | 0 | |
| 2.0039 | LSLDVSAAFY | 10 | HBV | ALL | POL | 1,000 | 1 | 4.2 | | <0.0009 | 0.0037 | |
| 1.0911 | FLCQQYLHLY | 10 | HBV | adr | POL | 1250 | 1 | 1.1 | 0.0025 | 0.014 | 0.0048 | 0.0017 |
| 2.0216 | QTFGRKLHLY | 10 | HBV | ayw | POL | 1087 | 1 | 1.1 | | 0.0056 | 0.012 | |
| 2.0244 | KTYGRKLHLY | 10 | HBV | adw | | 1,098 | 1 | 0.69 | 0.0003 | 0.59 | 0.22 | 0 |
| 1.0791 | KTYGRKLHLY | 10 | HBV | adw | POL | 1098 | 1 | 0.57 | 0.0000 | 0.53 | 0.35 | 0.0001 |
| 2.0242 | QTFGRKLHLY | 10 | HBV | ayw | | 1,087 | 1 | 0.37 | | 0.0037 | 0.011 | |
| 1.0556 | KTFGRKLHLY | 10 | HBV | adr | POL | 1069 | 1 | 0.34 | 0.0023 | 0.094 | 0.090 | 0 |
| 2.0241 | KTFGRKLHLY | 10 | HBV | adr | | 1,069 | 1 | 0.30 | 0.0002 | 0.15 | 0.095 | 0 |
| 1.0766 | LQDPRVRALY | 10 | HBV | adw | ENV | 120 | 1 | 0.21 | | 0.014 | 0 | |
| 1.0806 | TTPAQGTSMY | 10 | HBV | adw | ENV | 288 | 1 | 0.20 | | 0 | 0 | |
| 2.0240 | LSSTSRNINY | 10 | HBV | adr | | 1,035 | 1 | 0.20 | | <0.0009 | 0 | |
| 1.0541 | PLDKGIKPYY | 10 | HBV | adr | POL | 698 | 1 | 0.16 | | 0 | 0.017 | 0 |
| 2.0238 | HSASRCGSPY | 10 | HBV | ayw | | 767 | 1 | 0.15 | 0 | 0.019 | 0.017 | 0 |
| 1.0795 | FLTKQYLNLY | 10 | HBV | adw | POL | 1279 | 1 | 0.12 | | 0 | 0 | |
| 2.0237 | RSASRCGSPY | 10 | HBV | adr/adw | | 738 | 1 | 0.11 | 0 | 0.033 | 0.020 | 0 |
| 1.0774 | WLWGMDIDPY | 10 | HBV | adw | CORE | 416 | 1 | 0.0981 | | <0.0002 | <0.0002 | |
| 2.0233 | TTPAQGTSMY | 10 | HBV | ayw | | 288 | 1 | 0.0966 | | | | |
| 1.0542 | FTTLWKAGILY | 10 | HBV | adr | POL | 723 | 1 | 0.030 | | | | |
| 2.0231 | TSCPPICPGY | 10 | HBV | adr | | 226 | 1 | 0.0118 | | | | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2.0246 | KSVQILESLY | 10 | HBV | adw | | 1,161 | 1 | 0.016 | | | | |
| 1.0910 | NLYYSLLLLY | 10 | HBV | adr | POL | 1059 | 1 | 0.015 | | | | |
| 2.0089 | LLYQTFGRK | 9 | HBV | ayw | POL | 1084 | 3 | | | 1.8 | 0.64 | |
| 2.0116 | IMPARFYPK | 9 | HBV | ayw | | 713 | 3 | | | 0.99 | 1.5 | |
| 2.0082 | CLIQSPVRK | 9 | HBV | ayw | POL | 967 | 3 | | | 0.14 | 0.025 | |
| 5.0056 | SAICSVYRR | 9 | HBV | | POL | 531 | 3 | | | <0.0003 | 0.067 | |
| 2.0077 | HLHQDIIKK | 9 | HBV | ayw | POL | 686 | 3 | | | 0.041 | 0.0075 | |
| 2.0219 | SLPQEHIQK | 10 | HBV | ayw | POL | 1197 | 3 | | | 0.36 | 4.2 | |
| 2.0234 | SMIPSCCCTK | 10 | HBV | adr/adw | | 295 | 3 | | | 0.43 | 1.9 | |
| 2.0235 | SMYPSCCCTK | 10 | HBV | ayw | | 295 | 3 | | | 1.1 | 1.79 | |
| 5.0107 | QAPTSPTYK | 10 | HBV | | POL | 665 | 3 | | | 0.15 | 1.3 | |
| 2.0214 | LLLYQTFGRK | 10 | HBV | ayw | POL | 1083 | 3 | | | 0.89 | 0.021 | |
| 2.0245 | YMDDVVLGAK | 10 | HBV | ALL | | 1,123 | 3 | | | 0.16 | 0.0076 | |
| 5.0108 | TSAICSVYRR | 10 | HBV | | POL | 530 | 3 | | | 0.0006 | 0.013 | |
| 2.0094 | PTYKAFLCK | 9 | HBV | ayw | POL | 1263 | 11 | | | 0.030 | 0.085 | |
| 2.0068 | PTDLEAYFK | 9 | HBV | adw | "X" | 1552 | 11 | | | 0.0002 | 0.016 | |
| 2.0061 | KYTSFPWLL | 9 | HBV | ALL | | 1,230 | 24 | | | | | 3.6 |
| 2.0069 | LYAAVTNFL | 9 | HBV | adw | | 1,169 | 24 | | | | | 3.2 |
| 2.0046 | FYPNLTKYL | 9 | HBV | adr | | 689 | 24 | | | | | 2.1 |
| 2.0045 | LYSSTVPSF | 9 | HBV | adw/ayw | | 665 | 24 | | | | | 1.9 |
| 2.0048 | FYPKVTKYL | 9 | HBV | ayw | | 718 | 24 | | | | | 1.7 |
| 2.0049 | FYPNVTKYL | 9 | HBV | adw | | 718 | 24 | | | | | 1.6 |
| 2.0039 | LYSILSPFL | 9 | HBV | ayw | | 368 | 24 | | | | | 0.50 |
| 2.0044 | LYSSTVPVL | 9 | HBV | adr | | 636 | 24 | | | | | 0.37 |
| 2.0038 | LYNILSPFL | 9 | HBV | adr | | 368 | 24 | | | | | 0.34 |
| 2.0061 | NYRVSWFKF | 9 | HBV | ayw | | 991 | 24 | | | | | 0.18 |
| 2.0050 | HYFQTRHYL | 9 | HBV | adw/ayw | | 743 | 24 | | | | | 0.15 |
| 2.0047 | HYFKTRHYL | 9 | HBV | adr | | 714 | 24 | | | | | 0.057 |
| 2.0060 | GYPALMPLY | 9 | HBV | ALL | | 1,224 | 24 | | | | | 0.049 |
| 5.0063 | AYRPPNAPI | 9 | HBV | NUC/XNUCFUS | | 131 | 24 | | | | | 0.026 |
| 2.0054 | LYQTFGRKL | 9 | HBV | ayw | | 1,085 | 24 | | | | | 0.014 |
| 2.0043 | SYQHFRKLL | 9 | HBV | ayw | | 647 | 24 | | | | | 0.011 |
| 2.0181 | LYSHPIILGF | 10 | HBV | ALL | | 1,077 | 24 | | | | | 1.1 |
| 2.0182 | LYAAVTNFLL | 10 | HBV | adw | | 1,169 | 24 | | | | | 0.32 |
| 2.0188 | LYRPLLSLPF | 10 | HBV | adr | | 1,371 | 24 | | | | | 0.25 |
| 2.0174 | SYQHFRKLLL | 10 | HBV | ayw | | 647 | 24 | | | | | 0.16 |
| 2.0173 | SYQHFRKLLL | 10 | HBV | adr/adw | | 578 | 24 | | | | | 0.066 |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2.0176 | YYPEILVNHY | 10 | HBV | ayw | POL | 715 | 24 | | | | | 0.040 |
| 2.0172 | AYRPPNAPIL | 10 | HBV | ALL | | 521 | 24 | | | | | 0.022 |
| 2.0171 | GYRWMCLRRF | 10 | HBV | ALL | | 234 | 24 | | | | | 0.011 |
| 5.0115 | NFLLSLGIIL | 10 | HBV | | POL | 572 | 24 | | | | | 0.0099 |
| 1.0077 | YVSLMLLYK | 9 | HBV | adw | POL | 1090 | 3.11 | | | 0.31 | 7.4 | |
| 1.0189 | LLYKTFGRK | 9 | HBV | adr | POL | 1066 | 3.11 | | | 5.0 | 0.30 | |
| 1.0079 | LLYKTYGRK | 9 | HBV | adw | POL | 1095 | 3.11 | | | 2.5 | 0.40 | |
| 1.0070 | VTKYLPLDK | 9 | HBV | adw | POL | 722 | 3.11 | | | 0.014 | 1.3 | |
| 1.0176 | RDYLHTLWK | 9 | HBV | adr | POL | 719 | 3.11 | | | 1.2 | 0.010 | |
| 1.0067 | STVPSENPK | 9 | HBV | adw | POL | 668 | 3.11 | | | 0.021 | 0.93 | |
| 1.0215 | TTDLEAYFK | 9 | HBV | adr | "X" | 1523 | 3.11 | | | 0.006 | 0.92 | |
| 1.0048 | YVSLLLLYK | 9 | HBV | adr | POL | 1061 | 3.11 | | | 0.39 | 0.92 | |
| 1.0083 | PTYKAFLTK | 9 | HBV | adw | POL | 1274 | 3.11 | | | 0.17 | 0.71 | |
| 1.0087 | HLYPVARQR | 9 | HBV | adr | POL | 1257 | 3.11 | | | 0.54 | 0.0020 | |
| 1.0358 | STNRQLGRK | 9 | HBV | adw | ENV | 85 | 3.11 | | | 0.51 | 0.34 | |
| 1.0991 | ALRFTSARR | 9 | HBV | adr | "X" | 1488 | 3.11 | | | 0.44 | <0.0005 | |
| 1.0197 | PVNRPIDWK | 9 | HBV | adr | POL | 1197 | 3.11 | | | 0.080 | 0.41 | |
| 1.0369 | TVNERRLK | 9 | HBV | adw | POL | 703 | 3.11 | | | 0.016 | 0.40 | |
| 1.1041 | VVNHYRQTR | 9 | HBV | adw | POL | 740 | 3.11 | | | 0.030 | 0.33 | |
| 1.0152 | STTSTGPCK | 9 | HBV | adr | ENV | 277 | 3.11 | | | 0.011 | 0.29 | |
| 1.0213 | QYLPKLLHK | 9 | HBV | adr | "X" | 1505 | 3.11 | | | 0.10 | 0.28 | |
| 1.0172 | LTKYLPLDK | 9 | HBV | adr | POL | 693 | 3.11 | | | 0.0039 | 0.23 | |
| 1.0374 | CLHQSAVRK | 9 | HBV | adw | POL | 878 | 3.11 | | | 0.22 | 0.017 | |
| 1.0980 | VVDFSQFSR | 9 | HBV | adr | POL | 963 | 3.11 | | | 0.011 | 0.20 | |
| 1.0382 | PLYACIQAK | 9 | HBV | adw | POL | 1259 | 3.11 | | | 0.18 | 0.034 | |
| 2.0074 | YVNTNMGLK | 9 | HBV | ayw | CORE | 507 | 3.11 | | | 0.16 | 0.048 | |
| 1.0199 | PLYACIQSK | 9 | HBV | adr | POL | 1230 | 3.11 | | | 0.11 | 0.018 | |
| 1.0972 | RLADEGLNR | 9 | HBV | adr | POL | 601 | 3.11 | | | 0.10 | 0.025 | |
| 1.0976 | AVNHYFKTR | 9 | HBV | adr | POL | 711 | 3.11 | | | 0.0071 | 0.098 | |
| 1.0975 | RLKLIMPAR | 9 | HBV | adr | POL | 680 | 3.11 | | | 0.095 | 0.0002 | |
| 1.0977 | ILYKRETTR | 9 | HBV | adr | POL | 700 | 3.11 | | | 0.095 | <0.0005 | |
| 1.0993 | KVFVLGGCR | 9 | HBV | adr | "X" | 1548 | 3.11 | | | 0.042 | 0.082 | |
| 1.0165 | NYSIPWTHK | 9 | HBV | adr | POL | 421 | 3.11 | | | 0.072 | 0.076 | |
| 1.0982 | LLLYKTFGR | 9 | HBV | adr | POL | 1065 | 3.11 | | | 0.072 | 0.0045 | |
| 1.0978 | RLVFQTSTR | 9 | HBV | adr | POL | 757 | 3.11 | | | 0.048 | 0.0032 | |
| 1.0219 | FVLGGCRHK | 9 | HBV | adr | "X" | 1550 | 3.11 | | | 0.065 | 0.019 | |
| 1.1042 | RLVLQTSTR | 9 | HBV | adw | POL | 786 | 3.11 | | | 0.064 | 0.0002 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.1043 | MLLYKTYGR | 9 | HBV | adw | POL | 1094 | 3.11 | | | 0.061 | 0.0032 | |
| 1.0170 | TVNEKRRLK | 9 | HBV | adr | POL | 674 | 3.11 | | | 0.048 | 0.037 | |
| 1.1045 | NLYPVARQR | 9 | HBV | adw | POL | 1286 | 3.11 | | | 0.042 | 0.0011 | |
| 1.1046 | LPYRPTTGR | 9 | HBV | adw | POL | 1407 | 3.11 | | | 0.021 | 0 | |
| 1.0845 | LVSPGVWIR | 9 | HBV | adr | CORE | 509 | 3.11 | | | 0.0033 | 0.020 | |
| 1.0981 | LVGSSGLPR | 9 | HBV | adr | POL | 1022 | 3.11 | | | 0.0008 | 0.015 | |
| 1.0967 | HSCLTFGR | 9 | HBV | adr | CORE | 494 | 3.11 | | | 0.013 | 0.011 | |
| 1.1047 | SVPSRLPDR | 9 | HBV | adw | POL | 1424 | 3.11 | | | 0.0007 | 0.010 | |
| 1.0969 | SVPSHLPDR | 9 | HBV | adr | POL | 1395 | 3.11 | | | 0.0004 | 0.010 | |
| 1.0564 | TLPQEHIVLK | 10 | HBV | adr | POL | 1179 | 3.11 | | | 0.092 | 5.6 | |
| 2.0005 | TVPVRNPHWK | 10 | HBV | ayw | POL | 669 | 3.11 | | | 0.0067 | 4.2 | |
| 1.0543 | TLWKAGILYK | 10 | HBV | adr | POL | 724 | 3.11 | | | 3.5 | 1.0 | |
| 1.0807 | SMYPSCCCTK | 10 | HBV | ayw | ENV | 295 | 3.11 | | | 1.5 | 3.4 | |
| 1.1153 | RLPYRPTTGR | 10 | HBV | adw | POL | 1406 | 3.11 | | | 2.8 | 0.030 | |
| 1.0564 | STTDLEAYFK | 10 | HBV | adr | 'X' | 1522 | 3.11 | | | 0.0006 | 2.7 | |
| 1.0554 | LLLYKTRGRK | 10 | HBV | adr | POL | 1065 | 3.11 | | | 2.5 | 0.012 | |
| 1.0799 | TVNAHRNLPK | 10 | HBV | adw | 'X' | 1529 | 3.11 | | | 0.82 | 0.65 | |
| 1.0586 | EAYFKDCLFK | 10 | HBV | adr | 'X' | 1527 | 3.11 | | | 0.007 | 0.74 | |
| 1.1081 | LVVDFSQFSR | 10 | HBV | adr | POL | 962 | 3.11 | | | 0.0009 | 0.63 | |
| 1.0789 | MLLYKTYGRK | 10 | HBV | adw | POL | 1094 | 3.11 | | | 0.61 | 0.020 | |
| 1.0546 | TAYSHLSTSK | 10 | HBV | adr | POL | 858 | 3.11 | | | 0.26 | 0.092 | |
| 1.0562 | SLGIHLNPNK | 10 | HBV | adr | POL | 1150 | 3.11 | | | 0.20 | 0.078 | |
| 1.1152 | RLGLYRPLLR | 10 | HBV | adw | POL | 1397 | 3.11 | | | 0.19 | 0.0049 | |
| 1.0547 | VTGGVFLVDK | 10 | HBV | adr | POL | 943 | 3.11 | | | 0.035 | 0.17 | |
| 1.1150 | RLRTPRTPAR | 10 | HBV | adw | POL | 962 | 3.11 | | | 0.17 | 0.0002 | |
| 1.0581 | TVNGHQVLPK | 10 | HBV | adr | 'X' | 1500 | 3.11 | | | 0.073 | 0.092 | |
| 1.1091 | SLPFQPTTGR | 10 | HBV | adr | POL | 1377 | 3.11 | | | 0.077 | 0.043 | |
| 1.1072 | TLPETTVVRR | 10 | HBV | adr | CORE | 532 | 3.11 | | | <0.0003 | 0.075 | |
| 1.1089 | GTDNSVVLSR | 10 | HBV | adr | POL | 1320 | 3.11 | | | 0.025 | 0.072 | |
| 1.1071 | STLPETTVVR | 10 | HBV | adr | CORE | 531 | 3.11 | | | 0.0005 | 0.068 | |
| 2.0010 | KVTKYLPLDK | 10 | HBV | ayw | POL | 721 | 3.11 | | | 0.027 | 0.053 | |
| 1.1148 | STRHGDKSFR | 10 | HBV | adw | POL | 792 | 3.11 | | | 0.0057 | 0.038 | |
| 1.0935 | VLSCWWLQFR | 10 | HBV | adw | POL | 923 | 3.11 | | | 0.029 | 0.0087 | |
| 1.0781 | NVTKYLPLDK | 10 | HBV | adw | POL | 721 | 3.11 | | | <0.0004 | 0.023 | |
| 1.1092 | RVCCQLDPAR | 10 | HBV | adr | 'X' | 1422 | 3.11 | | | 0.0019 | 0.0123 | |
| 1.0793 | SLGIIILNPQK | 10 | HBV | adw | POL | 1179 | 3.11 | | | 0.017 | 0.0114 | |
| 1.0909 | YLVSRGVWIR | 10 | HBV | adr | CORE | 508 | 3.11 | | | 0.015 | 0.00127 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2.0207 | FVGPLTVNEK | 10 | HBV | ayw | POL | 498 | 3,11 | | | 0.0057 | 0.015 | |
| 1.0535 | YVGPLTVNEK | 10 | HBV | adr | POL | 669 | 3,11 | | | 0.0069 | 0.014 | |
| 1.1075 | RLADEGLNRR | 10 | HBV | adr | POL | 601 | 3,11 | | | 0.013 | 0.0004 | |
| 1.1086 | IVLKLKQCFR | 10 | HBV | adr | POL | 1185 | 3,11 | | | 0.013 | 0.0024 | |
| 1.0773 | PIPSSWAFAK | 10 | HBV | adw | ENV | 314 | 3,11 | | | <0.0003 | 0.010 | |
| 1.0778 | LTVNEKRRLK | 10 | HBV | adw | POL | 702 | 3,11 | | | 0.0025 | 0.0095 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0118 | CTCGSSDLY | 9 | HCV | | LORF | 1123 | 1 | 3.0 | | 0 | 0.010 | |
| 1.0112 | NIVDVQYLY | 9 | HCV | | NS1/ENV2 | 697 | 1 | 0.60 | | 0 | 0.010 | |
| 2.0034 | VQDCNCSIY | 9 | HCV | | | 302 | 1 | 0.54 | | 0.0005 | 0.0003 | |
| 2.0035 | LTPRCMVDY | 9 | HCV | | | 605 | 1 | 0.078 | | | | |
| 1.0145 | RVCEKMALY | 9 | HCV | | LORF | 2588 | 1 | 0.053 | | | | |
| 1.0140 | DVVCCSMSY | 9 | HCV | | LORF | 2416 | 1 | 0.039 | | | | |
| 2.0036 | FTIFKIRMY | 9 | HCV | | | 626 | 1 | 0.012 | | | | |
| 1.0509 | GLSAFSLHSY | 10 | HCV | | LORF | 2888 | 1 | 0.41 | 0.0002 | 0.013 | 0.0034 | 0.0002 |
| 1.0489 | TLHGPTPLLY | 10 | HCV | | LORF | 1617 | 1 | 0.30 | | 0.11 | 0.0024 | |
| 2.0037 | EYVLLLFLL | 9 | HCV | | | 719 | 24 | | | | | 1.4 |
| 2.0169 | MYVGGVEHRL | 10 | HCV | | | 633 | 24 | | | | | 0.026 |
| 2.0170 | EYVLLLFLLL | 10 | HCV | | | 719 | 24 | | | | | 0.010 |
| 1.0139 | SVPAEILRK | 9 | HCV | | LORF | 2269 | 3,11 | | | 0.016 | 0.87 | |
| 1.0955 | QLFTPSPRR | 9 | HCV | | ENV1 | 290 | 3,11 | | | 0.75 | 0.033 | |
| 1.0090 | RLGVRATRK | 9 | HCV | | CORE | 43 | 3,11 | | | 0.74 | 0.16 | |
| 1.0123 | LIFCHSKKK | 9 | HCV | | LORF | 1391 | 3,11 | | | 0.54 | 0.19 | |
| 1.0122 | HLIFCHSKK | 9 | HCV | | LORF | 1390 | 3,11 | | | 0.25 | 0.010 | |
| 1.0952 | KTSERSQPR | 9 | HCV | | CORE | 51 | 3,11 | | | 0.16 | 0.064 | |
| 1.0120 | AVCTRGVAK | 9 | HCV | | LORF | 1183 | 3,11 | | | 0.016 | 0.038 | |
| 1.0143 | EVFCVQPEK | 9 | HCV | | LORF | 2563 | 3,11 | | | 0.0019 | 0.033 | |
| 1.0137 | ITRVESENK | 9 | HCV | | LORF | 2241 | 3,11 | | | 0.015 | 0.0079 | |
| 1.0957 | CIITSLTGR | 9 | HCV | | LORF | 1042 | 3,11 | | | 0.0095 | 0.011 | |
| 1.0496 | GVAGALVAFK | 10 | HCV | | LORF | 1858 | 3,11 | | | 0.87 | 1.1 | |
| 1.0480 | HLHAPTGSGK | 10 | HCV | | LORF | 1227 | 3,11 | | | 0.57 | 0.0051 | |
| 1.1062 | RMYVGGVEHR | 10 | HCV | | NS1/ENV2 | 632 | 3,11 | | | 0.27 | 0.012 | |
| 1.0485 | HLIFCHSKKK | 10 | HCV | | LORF | 1390 | 3,11 | | | 0.27 | 0.025 | |
| 1.0484 | TLGFGAYMSK | 10 | HCV | | LORF | 1261 | 3,11 | | | 0.17 | 0.13 | |
| 1.1067 | GVGIYLLPNR | 10 | HCV | | LORF | 3002 | 3,11 | | | 0.0029 | 0.032 | |
| 1.1063 | LLFLLLADAR | 10 | HCV | | NS1/ENV2 | 723 | 3,11 | | | 0.015 | 0 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0014 | FRDYVDRFY | 9 | HIV | | GAG | 298 | 1 | 0.090 | | | | |
| 2.0129 | IYQYMDDLY | 9 | HIV | | | 875 | 1 | 0.064 | | | | |
| 1.0028 | TVLDVGDAY | 9 | HIV | | POL | 802 | 1 | 0.018 | | <0.0002 | 0.0056 | |
| 1.0412 | VTVLDVGDAY | 10 | HIV | | POL | 801 | 1 | 0.28 | | 0 | 0.0004 | |
| 1.0415 | VIYQYMDDLY | 10 | HIV | | POL | 874 | 1 | 0.25 | | 0.0007 | 0.0090 | |
| 2.0252 | VTVLDVGDAY | 10 | HIV | | | 801 | 1 | 0.088 | | | | |
| 1.0431 | EVNIVTDSQY | 10 | HIV | | POL | 1187 | 1 | 0.053 | | | | |
| 1.0441 | LVAVHVASGY | 10 | HIV | | POL | 1329 | 1 | 0.039 | | | | |
| 1.0442 | PAETGQETAY | 10 | HIV | | POL | 1345 | 1 | 0.013 | | | | |
| 2.0251 | ISKIGPENPY | 10 | HIV | | | 742 | 1 | 0.013 | | | | |
| 2.0255 | QMAVFIHNFK | 10 | HIV | | | 1,432 | 3 | | | 0.61 | 0.64 | |
| 2.0064 | RYLKDQQLL | 9 | HIV | | | 2,778 | 24 | | | | | 0.76 |
| 2.0134 | RYLKDQQLL | 9 | HIV | | | 2,778 | 24 | | | | | 0.32 |
| 2.0065 | TYQIYQEPF | 9 | HIV | | | 1,033 | 24 | | | | | 0.30 |
| 2.0131 | TYQIYQEPF | 9 | HIV | | | 1,033 | 24 | | | | | 0.20 |
| 2.0063 | IYQEPFKNL | 9 | HIV | | | 1,036 | 24 | | | | | 0.052 |
| 2.0132 | IYQEPFKNL | 9 | HIV | | | 1,036 | 24 | | | | | 0.033 |
| 2.0066 | IYQYMDDLY | 9 | HIV | | | 875 | 24 | | | | | 0.013 |
| 2.0247 | IYKRWIILGL | 10 | HIV | | | 266 | 24 | | | | | 0.017 |
| 2.0190 | IYKRWIILGL | 10 | HIV | | | 266 | 24 | | | | | 0.014 |
| 2.0249 | LYPLASLRSL | 10 | HIV | | | 506 | 24 | | | | | 0.014 |
| 1.0069 | KLAGRWPVK | 9 | HIV | | POL | 1358 | 3,11 | | | 2.7 | 0.069 | |
| 1.0944 | AVFIHNFKR | 9 | HIV | | POL | 1434 | 3,11 | | | 0.17 | 1.8 | |
| 1.0032 | AIPQSSMTK | 9 | HIV | | POL | 853 | 3,11 | | | 1.1 | 0.96 | |
| 1.0046 | IVIWGKTPK | 9 | HIV | | POL | 1075 | 3,11 | | | 0.085 | 0.37 | |
| 1.0079 | KLTEDRWNK | 9 | HIV | | VIF | 1712 | 3,11 | | | 0.013 | 0.27 | |
| 1.0027 | GIPHPAGLK | 9 | HIV | | POL | 788 | 3,11 | | | 0.23 | 0.065 | |
| 1.0059 | QIIEQLIKK | 9 | HIV | | POL | 1215 | 3,11 | | | 0.0091 | 0.16 | |
| 1.0939 | KIWPSYKGR | 9 | HIV | | GAG | 443 | 3,11 | | | 0.12 | 0.0005 | |
| 1.0072 | IIATDIQTK | 9 | HIV | | POL | 1458 | 3,11 | | | 0.025 | 0.098 | |
| 1.0036 | MGYELHPDK | 9 | HIV | | POL | 925 | 3,11 | | | 0.064 | 0.096 | |
| 1.0062 | YLAWVPAHK | 9 | HIV | | POL | 1227 | 3,11 | | | 0.077 | 0.057 | |
| 1.0938 | KIWPSHKGR | 9 | HIV | | GAG | 443 | 3,11 | | | 0.077 | <0.0005 | |
| 1.0047 | FVNTPPLVK | 9 | HIV | | POL | 1111 | 3,11 | | | 0.012 | 0.066 | |
| 1.0024 | NTPVFAIKK | 9 | HIV | | POL | 752 | 3,11 | | | 0.033 | 0.060 | |
| 1.0080 | TVQCTHGIK | 9 | HIV | | ENV | 2420 | 3,11 | | | 0.0021 | 0.046 | |
| 1.0013 | ILDIRQGPK | 9 | HIV | | GAG | 287 | 3,11 | | | 0.042 | 0.0048 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0015 | RDYVDRFYK | 9 | HIV | | GAG | 299 | 3,11 | | | 0.1007 | 0.040 | |
| 1.0058 | GIIQAQPDK | 9 | HIV | | POL | 1199 | 3,11 | | | <0.0009 | 0.040 | |
| 1.0064 | VLFLDGIDK | 9 | HIV | | POL | 1254 | 3,11 | | | 0.038 | 0.032 | |
| 1.0026 | LVDFRELNK | 9 | HIV | | POL | 769 | 3,11 | | | 0.011 | 0.030 | |
| 1.0078 | KVVPRRKAK | 9 | HIV | | POL | 1513 | 3,11 | | | 0.029 | 0.0039 | |
| 1.0942 | MTKILEPFR | 9 | HIV | | POL | 859 | 3,11 | | | <0.0008 | 0.016 | |
| 1.0463 | TVYYGVPVWK | 10 | HIV | | ENV | 2185 | 3,11 | | | 3.8 | 7.8 | |
| 1.0418 | TVQPIVLPEK | 10 | HIV | | POL | 935 | 3,11 | | | 0.16 | 5.6 | |
| 1.0447 | AVFIHNFKRK | 10 | HIV | | POL | 1434 | 3,11 | | | 0.66 | 0.85 | |
| 1.0437 | KVLFLDGIDK | 10 | HIV | | POL | 1253 | 3,11 | | | 0.36 | 0.78 | |
| 1.0408 | KLVDFRELNK | 10 | HIV | | POL | 768 | 3,11 | | | 0.51 | 0.090 | |
| 1.0403 | KLKPGMDGPK | 10 | HIV | | POL | 706 | 3,11 | | | 0.39 | 0.076 | |
| 1.0095 | FLGKIWPSYK | 10 | HIV | | GAG | 440 | 3,11 | | | 0.32 | 0.024 | |
| 1.1056 | KIQNFRVYYR | 10 | HIV | | POL | 1474 | 3,11 | | | 0.052 | 0.21 | |
| 1.0410 | GIPHPAGLKK | 10 | HIV | | POL | 788 | 3,11 | | | 0.011 | 0.17 | |
| 1.0426 | LVKLWYQLEK | 10 | HIV | | POL | 1117 | 3,11 | | | 0.056 | 0.082 | |
| 1.0098 | MIGGIGGFIK | 10 | HIV | | POL | 642 | 3,11 | | | 0.0099 | 0.055 | |
| 1.0413 | MTKILEPFRK | 10 | HIV | | POL | 859 | 3,11 | | | 0.015 | 0.038 | |
| 1.0433 | VVIQDNSDIK | 10 | HIV | | POL | 1504 | 3,11 | | | <0.0005 | 0.021 | |
| 1.0394 | FLGKIWPSHK | 10 | HIV | | GAG | 440 | 3,11 | | | 0.020 | 0.0013 | |
| 1.1059 | IVQQQNNLLR | 10 | HIV | | ENV | 2741 | 3,11 | | | 0.0024 | 0.019 | |
| 1.0417 | FTTPDKKHQK | 10 | HIV | | POL | 909 | 3,11 | | | <0.0002 | 0.015 | |
| 1.0405 | LVEICTEMEK | 10 | HIV | | POL | 729 | 3,11 | | | 0.0002 | 0.012 | |
| 1.0392 | LVQNANPDCK | 10 | HIV | | GAG | 327 | 3,11 | | | <0.0002 | 0.011 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0225 | LSEYRHYCY | 9 | HPV | 16 | E6 | 80 | 1 | 7.8 | | 0.0011 | 0.036 | |
| 1.0230 | QAEPDRAIIY | 9 | HPV | 16 | E7 | 44 | 1 | 0.021 | | <0.0002 | <0.0002 | |
| 1.0610 | LQDIETCVY | 10 | HPV | 18 | E6 | 25 | 1 | 0.25 | | 0.0056 | 0.012 | |
| 2.0159 | YSKISEYRHY | 10 | HPV | 16 | E6 | 77 | 1 | 0.17 | | <0.0009 | 0 | |
| 2.0162 | YSKSEYRHY | 10 | HPV | 16 | E6 | 77 | 1 | 0.11 | | <0.0009 | 0 | |
| 1.0599 | HGDTPTLHEY | 10 | HPV | 16 | E7 | 2 | 1 | 0.087 | | <0.0002 | <0.0002 | |
| 1.0601 | QPETTDLYCY | 10 | HPV | 16 | E7 | 16 | 1 | 0.033 | | | | |
| 1.0913 | IHDIILECVY | 10 | HPV | 16 | E6 | 30 | 1 | 0.032 | | | | |
| 1.0594 | AVCDKCLKFY | 10 | HPV | 16 | E6 | 68 | 1 | 0.0095 | | 0.0052 | 0.019 | |
| 2.0160 | YSKIRELRHY | 10 | HPV | 18 | E6 | 72 | 1 | 0.018 | | <0.0002 | <0.0002 | |
| 2.0161 | LLIRCLRCQK | 10 | HPV | 18 | E6 | 101 | 3 | 0.012 | | 0.081 | 0.078 | |
| 2.0032 | HTMLGMCCK | 9 | HPV | 18 | E7 | 59 | 11 | | | 0.020 | 0.079 | 0.33 |
| 2.0029 | VYCKTVLEL | 9 | HPV | 18 | E6 | 33 | 24 | | | | | 0.057 |
| 2.0027 | CYSLYGTTL | 9 | HPV | 16 | E6 | 87 | 24 | | | | | 0.032 |
| 2.0024 | VYDFAFRDL | 9 | HPV | 16 | E6 | 49 | 24 | | | | | 0.019 |
| 2.0081 | LYNLLIRCL | 9 | HPV | 18 | E6 | 98 | 24 | | | | | 0.010 |
| 2.0030 | VYGDTLEKL | 9 | HPV | 18 | E6 | 85 | 24 | | | | | |
| 1.0239 | SVYGDTLEK | 9 | HPV | 18 | E6 | 84 | 3,11 | | | 0.39 | 2.3 | |
| 1.0243 | SVYGDTLEK | 9 | HPV | 18 | E6 | 84 | 3,11 | | | 0.55 | 1.1 | |
| 1.0244 | SVYGDTLEK | 9 | HPV | 18 | E6 | 84 | 3,11 | | | 0.70 | 0.95 | |
| 1.0226 | TTLEQQYNK | 9 | HPV | 16 | E6 | 93 | 3,11 | | | 0.010 | 0.67 | |
| 1.0241 | SIPHAACHK | 9 | HPV | 18 | E6 | 59 | 3,11 | | | 0.0094 | 0.25 | |
| 1.0227 | SIPHAACHK | 9 | HPV | 18 | E6 | 59 | 3,11 | | | 0.017 | 0.12 | |
| 1.0233 | IVCPICSQK | 9 | HPV | 16 | E7 | 89 | 3,11 | | | 0.035 | 0.023 | |
| 1.0997 | KLRHLNEKR | 9 | HPV | 18 | E6 | 117 | 3,11 | | | 0.025 | <0.0005 | |
| 1.0234 | LLRCLRCQK | 9 | HPV | 18 | E6 | 102 | 3,11 | | | 0.019 | 0.0012 | |
| 1.0863 | IILECVYCK | 9 | HPV | 16 | E6 | 33 | 3,11 | | | 0.0016 | 0.019 | |
| 1.0999 | CIDFTSRIR | 9 | HPV | 18 | E6 | 68 | 3,11 | | | 0.017 | 0.0018 | |
| 1.0998 | CIDFYSRIR | 9 | HPV | 18 | E6 | 68 | 3,11 | | | 0.010 | 0.0009 | |
| 1.0596 | GTTLEQQYNK | 10 | HPV | 16 | E6 | 92 | 3,11 | | | 0.010 | 0.98 | |
| 1.0606 | LLIRCLRCQK | 10 | HPV | 18 | E6 | 101 | 3,11 | | | 0.076 | 0.29 | |
| 1.0598 | LLIRCINCQK | 10 | HPV | 16 | E6 | 106 | 3,11 | | | 0.12 | 0.24 | |
| 1.0629 | LLIRCLRCQK | 10 | HPV | 18 | E6 | 101 | 3,11 | | | 0.16 | 0.11 | |
| 1.0614 | LTEVFEFAFK | 10 | HPV | 18 | E6 | 41 | 3,11 | | | 0.0009 | 0.11 | |
| 1.0605 | GIVCPICSQK | 10 | HPV | 16 | E7 | 88 | 3,11 | | | 0.0017 | 0.040 | |
| 1.0625 | LTEVFEFAFK | 10 | HPV | 18 | E6 | 41 | 3,11 | | | 0.0012 | 0.041 | |
| 1.0591 | DIILECVYCK | 10 | HPV | 16 | E6 | 32 | 3,11 | | | 0.0065 | 0.021 | |
| 1.1101 | KLRHLNEKHR | 10 | HPV | 18 | E6 | 117 | 3,11 | | | 0.013 | 0 | |
| 1.1095 | CVYCKQQLLR | 10 | HPV | 16 | E6 | 37 | 3,11 | | | 0.011 | 0.0059 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2.0020 | EVDPIGHLY | 9 | MAGE | 3 | | 161 | 1 | 18 | | 0.0002 | 0.0009 | |
| 3.0172 | EADPTSNTY | 9 | MAGE | 5/51 | | 161 | 1 | 9.9 | | 0.0006 | 0.0006 | 0 |
| 1.0259 | TQDLVQEKY | 9 | MAGE | 1 | | 240 | 1 | 2.1 | 0 | 0.0002 | | |
| 3.0173 | EVDPIGHVY | 9 | MAGE | 6 | | 161 | 1 | 1.9 | <0.0002 | <0.0002 | 0 | |
| 1.0254 | EADPTGHSY | 9 | MAGE | 1 | | 161 | 1 | 1.1 | 0 | 0 | | |
| 1.0259 | LVQEKYLEY | 9 | MAGE | 1 | | 243 | 1 | 0.42 | 0.0013 | 0.003 | | |
| 6.0003 | TSYVKVLEY | 9 | MAGE | 1 | new | 275 | 1 | 0.099 | | | | |
| 2.0009 | SSLPTMGNY | 9 | MAGE | 3 | | 9 | 1 | 0.055 | | | | |
| 2.0011 | GSVGNPWQY | 9 | MAGE | 3 | | 77 | 1 | 0.050 | | | | |
| 2.0008 | SSRSTLNNY | 9 | MAGE | 2 | | 9 | 1 | 0.043 | | | | |
| 1.0253 | MLESVTKNY | 9 | MAGE | 1 | | 128 | 1 | 0.011 | | | | |
| 2.0147 | ASSLPTMNY | 10 | MAGE | 3 | | 8 | 1 | 2.6 | <0.0009 | 0.003 | | |
| 2.0147 | LTQDLVQEKY | 10 | MAGE | 1 | | 239 | 1 | 1.2 | <0.0009 | 0.0073 | | |
| 6.0114 | ETSYVKVLEY | 10 | MAGE | 1 | new | 274 | 1 | 0.56 | | | | |
| 2.0141 | ASSRTLNNY | 10 | MAGE | 2 | | 8 | 1 | 0.17 | <0.0009 | 0.026 | | |
| 1.0648 | DLVQEKYLEY | 10 | MAGE | 1 | | 242 | 1 | 0.094 | | | | |
| 6.0046 | TSYVKVLEY | 9 | MAGE | 1 | new | 275 | 3 | | 0.71 | 0.010 | | |
| 6.0119 | TDNFTRGK | 9 | MAGE | 1 | | 66 | 3 | | 0.043 | 0.37 | | |
| 6.0044 | ALAETSYVK | 9 | MAGE | 1 | new | 271 | 3 | | 0.31 | 0.36 | | |
| 6.0132 | LTQDLVQEK | 9 | MAGE | 1 | | 239 | 3 | | <0.0003 | 0.14 | | |
| 6.0043 | LVQEKYLEY | 9 | MAGE | 1 | new | 243 | 3 | | 0.0026 | 0.004 | | |
| 6.0131 | MLAYCGPRK | 9 | MAGE | 1 | | 229 | 3 | | 0.014 | 0.0009 | | |
| 6.0122 | LPRAVITGK | 9 | MAGE | 1 | | 97 | 3 | | 0.011 | 0.0005 | | |
| 6.0124 | EVDPIGHSY | 10 | MAGE | 1 | new | 290 | 3 | | 0.43 | 0.0009 | | |
| 6.0161 | ADLVGFLLLK | 10 | MAGE | 1 | | 107 | 3 | | 0.35 | 0.29 | | |
| 6.0160 | ESLPRAVITK | 10 | MAGE | 1 | | 95 | 3 | | 0.14 | 0.098 | | |
| 6.0119 | DLVQEKYLEY | 10 | MAGE | 1 | new | 242 | 3 | | 0.002 | 0.0051 | | |
| 6.0123 | YVKVKAAIVR | 10 | MAGE | 1 | new | 283 | 3 | | 0.019 | 0.0009 | | |
| 6.0144 | LSYMEYTDGR | 10 | MAGE | 1 | | 218 | 3 | | <0.0003 | 0.012 | | |
| 6.0143 | KAEMLESVIK | 10 | MAGE | 1 | | 125 | 3 | | <0.0003 | 0.0097 | | |
| 6.0125 | RALAETSYVK | 10 | MAGE | 1 | new | 270 | 11 | | 0.18 | 0.24 | | |
| 2.0010 | NYPLWSQSY | 9 | MAGE | 3 | | 16 | 24 | | | | 0.027 | |
| 2.0149 | NYKHCFPEP | 10 | MAGE | 1 | | 135 | 24 | | | | 0.25 | |
| 2.0151 | LYPAFCLGL | 10 | MAGE | 3 | | 115 | 24 | | | | 0.048 | |
| 6.0126 | SYVKVLEYV | 10 | MAGE | 1 | new | 274 | 24 | | | | 0.004 | |
| 1.0248 | SLPRAVITK | 9 | MAGE | 1 | | 96 | 3.11 | | | 4.1 | 2.7 | |
| 1.1006 | SYAEYTDGR | 9 | MAGE | 1 | | 219 | 3.11 | | | 0.0099 | 1.3 | |
| 1.1004 | TTDNFTRGR | 9 | MAGE | 1 | | 66 | 3.11 | | | 0.016 | 1.0 | |
| 1.0257 | LTQDLVQEK | 9 | MAGE | 1 | | 239 | 3.11 | | | 0.0002 | 0.38 | |
| 1.0434 | SLPRAVITGK | 10 | MAGE | 1 | | 96 | 3.11 | | | 1.2 | 0.98 | |
| 1.0447 | LLTQDLVQEK | 10 | MAGE | 1 | | 238 | 3.11 | | | 0.0004 | 0.16 | |
| 1.0440 | MLESVTKNYK | 10 | MAGE | 1 | | 128 | 3.11 | | | 0.14 | 0.027 | |
| 1.0444 | LLGDNQIMPK | 10 | MAGE | 1/3 | | 182 | 3.11 | | | 0.020 | 0.011 | |
| 1.0430 | SLEQRSLHCK | 10 | MAGE | 1 | | 2 | 3.11 | | | 0.015 | 0.015 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0281 | CSDCTTIIY | 9 | p53 | | | 226 | 1 | 29.5 | | 0.0010 | 0.029 | |
| 1.0667 | CTAKSVTCTY | 10 | p53 | | | 117 | 1 | 0.33 | 0 | 0.023 | 0.049 | 0 |
| 1.0672 | RVEGNLRVEY | 10 | p53 | | | 196 | 1 | 0.022 | | 0.0014 | 0.0020 | |
| 1.0278 | RVRAMAIYK | 9 | p53 | | | 156 | 3,11 | | | 1.5 | 0.73 | |
| 1.0276 | CTYSPALNK | 9 | p53 | | | 124 | 3,11 | | | 0.46 | 1.1 | |
| 1.0285 | NTSSSPQPK | 9 | p53 | | | 311 | 3,11 | | | 0.0009 | 0.095 | |
| 1.0284 | RTEEENLRK | 9 | p53 | | | 283 | 3,11 | | | 0.0015 | 0.091 | |
| 1.0287 | ELNEALELK | 9 | p53 | | | 343 | 3,11 | | | 0.020 | 0.0052 | |
| 1.0678 | RTEEENLRKK | 10 | p53 | | | 283 | 3,11 | | | 3.3 | 0.0080 | |
| 1.1113 | KTYQGSYGFR | 10 | p53 | | | 101 | 3,11 | | | 2.6 | 0.88 | |
| 1.1115 | VVRRCPHHER | 10 | p53 | | | 172 | 3,11 | | | 0.099 | 0.0017 | |
| 1.0679 | NTSSSPQPKK | 10 | p53 | | | 311 | 3,11 | | | 0.0035 | 0.054 | |
| 1.1121 | RVCACPGRDR | 10 | p53 | | | 273 | 3,11 | | | 0.014 | 0.011 | |
| 1.1116 | GLAPPQHLIR | 10 | p53 | | | 187 | 3,11 | | | 0.013 | 0.0006 | |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 3.0175 | KGEYFVEMY | 9 | PAP | | | 322 | 1 | 3.4 | | <0.0002 | 0.0002 | 0 |
| 3.0174 | LGEYIRKRY | 9 | PAP | | | 81 | 1 | 0.78 | | <0.0002 | 0.0002 | 0 |
| 3.0166 | ASCHLTELY | 9 | PAP | | | 311 | 1 | 0.77 | <0.0002 | <0.0002 | 0.055 | 0 |
| 3.0163 | ESYKHEQVY | 9 | PAP | | | 95 | 1 | 0.098 | | <0.0002 | 0.0002 | 0 |
| 3.0237 | LSELSLLSLY | 10 | PAP | | | 238 | 1 | 14 | | 0.0026 | 0.0004 | 0 |
| 3.0235 | LSELSLLSLY | 10 | PAP | | | 238 | 1 | 12 | | 0.0005 | 0.0004 | 0 |
| 3.0236 | LTQLGMEQHY | 10 | PAP | | | 70 | 1 | 0.62 | 0.0005 | 0.015 | 0.0024 | 0.0022 |
| 3.0238 | KGEYFVEMYY | 10 | PAP | | | 322 | 1 | 0.018 | | 0.0057 | 0.089 | |
| 3.0230 | LVNEILNHMK | 10 | PAP | | | 263 | 3 | | | 0.056 | 0.12 | |
| 3.0158 | ATQIPSYKK | 9 | PAP | | | 274 | 11 | | | 0.10 | 1.2 | |
| 3.0231 | ETLKSEERQK | 10 | PAP | | | 170 | 11 | | | <0.0004 | 0.014 | |
| 3.0161 | LYFEKGEYF | 9 | PAP | | | 318 | 24 | | | | | 2.5 |
| 3.0160 | LYCESVHNF | 9 | PAP | | | 213 | 24 | | | | | 0.44 |
| 3.0159 | PYKDFIATL | 9 | PAP | | | 183 | 24 | | | | | 0.11 |
| 3.0162 | VYNGLLPPY | 9 | PAP | | | 302 | 24 | | | | | 0.032 |
| 3.0232 | PYASCHLTEL | 10 | PAP | | | 309 | 24 | | | | | 0.024 |

| Peptide | Sequence | AA | Virus | Strain | Molecule | Pos. | Motif | A1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1.0270 | ALFEKPELY | 9 | FSA | | | 231 | 1 | 0.011 | | | |
| 2.0137 | VSHSPYHPLY | 10 | FSA | | | 88 | 1 | 0.15 | <0.0003 | 0.0015 | |
| 1.0265 | FLYDMSLLK | 9 | FSA | | | 95 | 3.11 | | 0.34 | 0.037 | |
| 1.0273 | VVHYYEKWIK | 9 | FSA | | | 242 | 3.11 | | 0.0072 | 0.083 | |
| 1.0272 | YTKVVHYEK | 9 | FSA | | | 209 | 3.11 | | 0.0036 | 0.038 | |
| 1.1039 | SLLKNEFLR | 9 | FSA | | | 100 | 3.11 | | 0.0024 | 0.017 | |
| 1.0260 | IVCGNWECK | 9 | FSA | | | 21 | 3.11 | | 0.041 | 0.019 | |
| 1.0269 | QVHPQKVYK | 9 | FSA | | | 182 | 3.11 | | 0.0060 | 0.014 | |
| 1.1112 | SLYTKVVHYR | 10 | FSA | | | 227 | 3.11 | | 0.38 | 0.25 | |
| 1.0263 | LTAAHCIRNK | 10 | FSA | | | 57 | 3.11 | | 0.14 | 0.083 | |
| 1.0261 | IIVCGWECEK | 10 | FSA | | | 20 | 3.11 | | 0.016 | 0.017 | |
| 1.0262 | KVVHYEKWIK | 10 | FSA | | | 241 | 3.11 | | 0.015 | 0.015 | |
| 1.1111 | VTKPMLCAGR | 10 | FSA | | | 188 | 3.11 | | 0.0033 | 0.017 | |
| 3.0109 | MLLRLSEPA | 9 | FSA | | | 118 | Random | | | | |

Table 5

| Sequence | Size | Antigen | Strain | Molecule | Freq | Pos. | Motif | A01 | A03 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Bind. | Bind. | Bind. | Bind. |
| EDTPIGHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 12.5000 | | | |
| AVDPIGHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 8.0000 | | | |
| EVDPIAHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 5.5000 | | | |
| FSPAFDNLYY | 10 | HER-2/neu | | | | 1213 | A01 | 5.5000 | 0.0005 | 0.0010 | |
| EVDAIGHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 5.3500 | | | |
| EVDPIGALY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 5.0000 | | | |
| EVDPIGHAY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 4.6500 | | | |
| EADPIGHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 3.4500 | | | |
| EVDPTGHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 2.9500 | | | |
| EVDPIGHSY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 2.6667 | | | |
| EVDPAGHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 2.4000 | | | |
| EVDPASNTY | 9 | MAGE | 4 | | | 161 | A01 | 1.5000 | | | |
| PLSEDQLLY | 9 | PAP | | | | 147 | A01 | 1.2000 | 0.0005 | 0.0001 | |
| LSAFSLHSY | 9 | HCV | | | | 2889 | A01 | 0.8100 | 0.0002 | 0.0002 | |
| IPSYKKLIMY | 10 | PAP | | | | 277 | A01 | 0.5650 | | | |
| YASCHLTELY | 10 | PAP | | | | 310 | A01 | 0.5467 | 0.0003 | 0.0002 | |
| EVDPIGHLA | 9 | MAGE3a | 3 | analog | | 161 | A01 | 0.3300 | | | |
| CMQIAKGMSY | 10 | HER-2/neu | | | | 826 | A01 | 0.2967 | 0.0003 | 0.0001 | |
| VGSDCTTIHY | 10 | p53 | | | | 225 | A01 | 0.2600 | 0.0003 | 0.0003 | |
| EVAPIGHLY | 9 | MAGE3a | 3 | analog | | 161 | A01 | 0.1800 | | | |

Table 5

| Sequence | Size | Antigen | Strain | Molecule | Freq | Pos. | Motif | A01 Bind. | A03 Bind. | A11 Bind. | A24 Bind. |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ESMPNPEGRY | 10 | HER-2/neu | | | | 280 | A01 | 0.1800 | 0.0003 | 0.0003 | |
| ASCVTACPY | 9 | HER-2/neu | | | | 293 | A01 | 0.0552 | 0.0008 | 0.0074 | |
| FSPAFDNLY | 9 | HER-2/neu | | | | 1213 | A01 | 0.0425 | 0.0002 | 0.0002 | |
| ASPLDSTFY | 9 | HER-2/neu | | | | 997 | A01 | 0.0290 | 0.0002 | 0.0004 | |
| RGTQLFENDY | 10 | HER-2/neu | | | | 103 | A01 | 0.0205 | 0.0003 | 0.0015 | |
| PASPLDSTFY | 10 | HER-2/neu | | | | 996 | A01 | 0.0148 | 0.0003 | 0.0001 | |
| PSQKTYQGSY | 10 | p53 | | | | 98 | A01 | 0.0140 | 0.0003 | 0.0003 | |
| KSTKVPAAY | 9 | HCV | | | | 1236 | A01 | 0.0134 | 0.0009 | 0.0001 | |
| DSSVLCECY | 9 | HCV | | | | 1513 | A01 | 0.0110 | 0.0002 | 0.0003 | |
| KISEYRHYCY | 10 | HPV | 16 | E6 | | 79 | A01 | 0.0090 | 0.0043 | 0.0038 | |
| NLYVSLMLLY | 10 | HBV | adw | POL | 20 | 1088 | A01 | 0.0090 | | | |
| GTRVRAMAIY | 10 | p53 | | | | 154 | A01/03 | 0.0027 | 0.0365 | 0.0002 | |
| LTCGFADLMGY | 11 | HCV | | | | 126 | A01/11 | 2.4500 | 0.0003 | 0.0120 | 0.0001 |
| VHAGVGSPY | 9 | HER-2/neu | | | | 773 | A01/A03 | 0.0400 | 0.0575 | 0.0079 | |
| TLWKAGILY | 9 | HBV | adr | POL | 100 | 724 | A03 | 0.0017 | 0.2667 | 0.0016 | |
| KLNWASQIY | 9 | HIV | | POL | | 958 | A03 | 0.0070 | 0.1160 | 0.0006 | |
| LVGFLLLKY | 9 | MAGE1 | 1 | | | 109 | A03 | 0.0033 | 0.0563 | 0.0012 | |
| ILRGTSFVY | 9 | HBV | adr | POL | 80 | 1345 | A03 | 0.0017 | 0.0440 | 0.0002 | |
| RVLQGLPREY | 10 | HER-2/neu | | | | 545 | A03 | 0.0015 | 0.0350 | 0.0050 | |

Table 5

| Sequence | Size | Antigen | Strain | Molecule | Freq | Pos. | Motif | A01 | A03 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Bind. | Bind. | Bind. | Bind. |
| QLVTQLMPY | 9 | HER-2/neu | | | | 795 | A03 | 0.0024 | 0.0112 | 0.0039 | |
| GLNKIVRMY | 9 | HIV | | GAG | | 274 | A03 | 0.0017 | 0.0103 | 0.0002 | |
| LLGDNQVMPK | 10 | MAGE2 | 2 | | | 182 | A03 | | 0.0093 | 0.0014 | |
| QVRDQAEHLK | 10 | HIV | | POL | | 1419 | A03 | | 0.0089 | 0.0093 | |
| LVSAGIRK | 8 | HIV | con | | | 1246 | A03 | | 0.0091 | 0.0054 | |
| VTDRGRQK | 8 | HIV | con | | | 1153 | A03 | | 0.0090 | 0.0065 | |
| TVFDAKRLIGR | 11 | HLA-Aw68 endogenous peptide sequences | | | | | A03/11 | | 0.1050 | 1.3000 | |
| KTGGPIYKR | 9 | HLA-Aw68 endogenous peptide sequences | | | | | A03/11 | | 0.0340 | 0.8200 | |
| SLYTKVVHY | 9 | PSA | | | | 237 | A03/11 | 0.0017 | 0.6750 | 0.0140 | |
| AVAAVAARR | 9 | HLA-Aw68 endogenous peptide sequences | | | | | A03/11 | | 0.1600 | 0.0825 | |
| KIQNFRVYY | 9 | HIV | | POL | | 1474 | A03/11 | 0.0056 | 0.1190 | 0.1350 | |
| EMLESVIKNYK | 11 | MAGE1 | | | | 127 | A03/11 | | 0.0087 | 0.0099 | |
| EVAPPEYHRK | 10 | HLA-Aw68 endogenous peptide sequences | | | | | A11 | | 0.0008 | 0.0575 | |
| ETAYFLLK | 8 | HIV | consensus | | | 1351 | A11 | | 0.0037 | 0.0425 | |
| RWGLLLALL | 9 | HER-2/neu | | | | 8 | A24 | | | | 1.2567 |
| PYVSRLLGI | 9 | HER-2/neu | | | | 780 | A24 | | | | 0.1650 |
| VYMIMVKCW | 9 | HER-2/neu | | | | 951 | A24 | | | | 0.1640 |
| AYSLTLQGL | 9 | HER-2/neu | | | | 440 | A24 | | | | 0.1250 |
| SYGVTVWEL | 9 | HER-2/neu | | | | 907 | A24 | | | | 0.1200 |
| LYISAWPDSL | 10 | HER-2/neu | | | | 410 | A24 | | | | 0.0835 |
| VWSYGVTVW | 9 | HER-2/neu | | | | 905 | A24 | | | | 0.0800 |

Table 5

| Sequence | Size | Antigen | Strain | Molecule | Freq | Pos. | Motif | A01 | A03 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Bind. | Bind. | Bind. | Bind. |
| SYGVTVWELM | 10 | HER-2/neu | | | | 907 | A24 | | | | 0.0630 |
| QYLAGLSTL | 9 | HCV | | | | 1777 | A24 | | | | 0.0475 |
| TYLPTNASL | 9 | HER-2/neu | | | | 63 | A24 | | | | 0.0375 |
| EYLVSFGVWI | 10 | HBV | | NUC | 90 | 117 | A24 | | | | 0.0335 |
| KFMLCAGRW | 9 | PSA | | | | 190 | A24 | | | | 0.0305 |
| WFHISCLTF | 9 | HBV | | NUC | 90 | 102 | A24 | | | | 0.0300 |
| TYSTYGKFL | 9 | HCV | | | | 1296 | A24 | | | | 0.0225 |
| VYMIMVKCWM | 10 | HER-2/neu | | | | 951 | A24 | | | | 0.0218 |
| RFRELVSEF | 9 | HER-2/neu | | | | 968 | A24 | | | | 0.0180 |
| CYGLGMEHL | 9 | HER-2/neu | | | | 342 | A24 | | | | 0.0176 |
| QYSPGQRVEF | 10 | HCV | | | | 2614 | A24 | | | | 0.0175 |
| KWMALESIL | 9 | HER-2/neu | | | | 887 | A24 | | | | 0.0149 |
| EYLVPQQGFF | 10 | HER-2/neu | | | | 1022 | A24 | | | | 0.0120 |
| RYSEDPTVPL | 10 | HER-2/neu | | | | 1111 | A24 | | | | 0.0117 |
| RFTHQSDVW | 9 | HER-2/neu | | | | 898 | A24 | | | | 0.0107 |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| DLVGFLLLK | 9 | 1 | | 108 | 3,11 | | | 0.0040 | 0.0014 | |
| QLVFGIDVK | 9 | 1 | | 152 | 3,11 | | | 0.0019 | 0.0051 | |
| SLEQRSLHCK | 10 | 1 | | 2 | 3,11 | | | 0.015 | 0.015 | |
| SLFRAVITKK | 10 | 1 | | 96 | 3,11 | | | 1.2 | 0.98 | |
| DLVGFLLLKY | 10 | 1 | | 108 | 1 | 0.0068 | | 0.0069 | 0.0009 | |
| MLESVIKNYK | 10 | 1 | | 128 | 3,11 | | | 0.14 | 0.027 | |
| WEELSVMEVY | 10 | 1 | | 215 | 1 | <0.0009 | | <0.0002 | <0.0002 | |
| VYDGREHSAY | 10 | 1 | | 223 | 1 | <0.0009 | | | | |
| LVGFLLLKY | 9 | 1 | | 109 | 1 | 0.0033 | | 0.056 | 0.0012 | |
| LVTCLGLSY | 9 | 1 | | 171 | 1 | 0.0084 | | 0.0014 | <0.0002 | |
| VLVTCLGLSY | 10 | 1 | | 170 | 1 | 0.0048 | 0 | 0.0013 | 0.0007 | |
| FLLLKYRAR | 9 | 1/2/3 | | 112 | 3,11 | | | 0.0007 | <0.0005 | |
| PTTINFTRQR | 10 | 1 | | 65 | 3,11 | | | <0.0002 | 0.0033 | |
| LVGFLLLKYR | 10 | 1 | | 109 | 3,11 | | | 0.0034 | 0.0023 | |
| EKYLEYGRCR | 10 | 1 | | 246 | 3,11 | | | <0.0002 | 0 | |
| ELVHFLLLK | 9 | 2/3 | | 108 | 3 | | | 0.0045 | 0.0011 | |
| AYGEPRKLL | 9 | 1 | | 231 | 24 | | | | | 0.0007 |
| SYVLVTCLGL | 10 | 1 | | 168 | 24 | | 0.0006 | | | 0.0051 |
| EVVPISHLY | 9 | 2 | | 161 | 1 | 0.0028 | | <0.0002 | <0.0002 | |
| EVVRIGHLY | 9 | 21 | | 161 | 1 | 0.0002 | | | | |
| EVDPASNTY | 9 | 4 | | 161 | 1 | 0.0005 | | | | |
| EADPTSNTY | 9 | 5/51 | | 161 | 1 | 9.9 | | 0.0006 | 0.0006 | 0 |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| EVDPIGHVY | 9 | 6 | | 161 | 1 | 1.9 | | <0.0002 | <0.0002 | 0 |
| EMLESVIK | 8 | 1 | | 127 | 3 | | | <0.0003 | 0 | |
| LVFGIDVK | 8 | 1 | | 153 | 3 | | | 0.0035 | 0.0037 | |
| GVQGPSLK | 8 | 1 | | 266 | 3 | | | <0.0003 | 0.0063 | |
| VMEVYDGR | 8 | 1 | | 220 | 3 | | | <0.0003 | 0.0007 | |
| VQEKYLEY | 8 | 1 | | 244 | 1 | 0.0018 | | | | |
| AYGEPRKL | 8 | 1 | | 231 | 24 | | | | | 0.0017 |
| VKEADPTGHSY | 11 | 1 | | 159 | 1 | <0.0003 | | | | |
| IWEELSVMEVY | 11 | 1 | | 214 | 1 | <0.0003 | | | | |
| EMLESVIKNYK | 11 | 1 | | 127 | 3 | | 0.0087 | 0.0099 | | |
| EADPTSHTY | 9 | analog | | 161 | 1 | 0.68 | | | | |
| EVDPTSNTY | 9 | analog | | 161 | 1 | 1.8 | | | | |
| EALEAQQEA | 9 | 1 | | 14 | 2.1 | | 0 | <0.0002 | 0 | |
| HSLEQRSLH | 9 | 1 | | 1 | 3 | | | 0.0025 | 0.0003 | |
| QSPQGASAF | 9 | 1 | | 56 | 3 | | | 0.0004 | 0 | |
| SAFPTTINF | 9 | 1 | | 62 | 3 | | | <0.0003 | 0 | 0.0003 |
| TSCILESLF | 9 | 1 | | 90 | 3 | | | <0.0003 | 0 | |
| SCILESLFR | 9 | 1 | | 91 | 3 | | | <0.0003 | 0.0026 | |
| LFRAVITKK | 9 | 1 | | 97 | 3 | | | 0.011 | 0.0005 | |
| VGFLLLKYR | 9 | 1 | | 110 | 3 | | | 0.0044 | 0.0051 | |
| ESVIKNYKH | 9 | 1 | | 130 | 3 | | | <0.0003 | 0 | |
| VIKNYKHCF | 9 | 1 | | 132 | 3 | | | <0.0003 | 0 | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| ASESLQLVF | 9 | 1,2 | | 147 | 3 | | | <0.0003 | 0 | |
| LGDNQIMPK | 9 | 1 | | 183 | 3 | | | 0.0007 | 0.0048 | |
| VMIAMEGGH | 9 | 1 | | 200 | 3 | | | <0.0003 | 0 | |
| YDGREHSAY | 9 | 1 | | 224 | 3 | | | <0.0003 | 0 | |
| LTQDLVQEK | 9 | 1 | | 239 | 3 | | | <0.0003 | 0.14 | |
| CGVQGPSLK | 9 | 1 | | 265 | 3 | | | <0.0003 | 0.0037 | |
| EMLESVIKNY | 10 | 1 | | 127 | 1 | 0.0006 | | <0.0002 | <0.0002 | 0 |
| KEADPTGHSY | 10 | 1 | | 160 | 1 | <0.0005 | | <0.0002 | <0.0002 | |
| ASAFPTTINF | 10 | 1 | | 61 | 3 | | | <0.0003 | <0.0002 | |
| AFPTTINFTR | 10 | 1 | | 63 | 3 | | | <0.0003 | 0.0003 | |
| PTTINFTRQR | 10 | 1 | | 65 | 3 | | | <0.0003 | 0.0002 | |
| STSCILESLF | 10 | 1 | | 89 | 3 | | | <0.0003 | <0.0002 | |
| GFLLLKYRAR | 10 | 1 | | 111 | 3 | | | 0.0019 | 0.0008 | |
| KAEMLESVIK | 10 | 1 | | 125 | 3 | | | <0.0003 | 0.0097 | |
| SVIKNYKHCF | 10 | 1 | | 131 | 3 | | | <0.0003 | <0.0002 | |
| KASESLQLVF | 10 | 1 | | 146 | 3 | | | <0.0003 | <0.0002 | 0.0012 |
| DVKEADPTGH | 10 | 1 | | 158 | 3 | | | <0.0003 | <0.0002 | |
| LVMIAMEGGH | 10 | 1 | | 199 | 3 | | | 0.0008 | 0.0005 | |
| LSVMEVYDGR | 10 | 1 | | 218 | 3 | | | <0.0003 | 0.012 | |
| VMEVYDGREH | 10 | 1 | | 220 | 3 | | | <0.0003 | 0.0002 | 0 |
| YGRCRTVIPH | 10 | 1 | | 251 | 3 | | | <0.0003 | <0.0002 | |
| SCGVQGPSLK | 10 | 1 | | 264 | 3 | | | 0.0005 | 0.0089 | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| VPDSDPARY | 9 | 1 | new | 254 | 1 | 0.0038 | | | | |
| QVPDSDPAR | 9 | 1 | new | 254 | 3 | | | <0.0003 | 0.0002 | |
| VIKVSARVR | 9 | 1 | new | 284 | 3 | | | 0.0016 | 0 | |
| PSLREAALR | 9 | 1 | new | 296 | 3 | | | <0.0003 | 0 | |
| EFLWGPRAL | 9 | 1 | new | 264 | 24 | | | | | 0.0006 |
| ETSYVKVLEY | 10 | 1 | new | 274 | 1 | 0.56 | | | | |
| LVQEKYLEYR | 10 | 1 | new | 243 | 3 | | | 0.0008 | 0.0043 | |
| QVPDSDPARY | 10 | 1 | new | 254 | 3 | | | 0.0014 | 0.0003 | |
| YVKVLEYVIK | 10 | 1 | new | 277 | 3 | | | 0.0029 | 0.0015 | |
| YVIKVSARVR | 10 | 1 | new | 283 | 3 | | | 0.019 | 0.0009 | |
| RALAETSYVK | 10 | 1 | new | 270 | 11 | | | 0.18 | 0.24 | |
| SYVKVLEYVI | 10 | 1 | new | 276 | 24 | | | | | 0.036 |
| FFPSLREAAL | 10 | 1 | new | 294 | 24 | | | | | 0.0044 |
| SVIKNYK | 7 | 1 N | POL | 131 | 3,11 | | | 0.0006 | 0.0028 | |
| PVTKAEMLESVIK | 13 | 1 n | E6 | 122 | 3,11 | | | <0.0003 | 0 | |
| ETSYVKVLEYVIK | 13 | 1 n | E6 | 273 | 3,11 | | | 0.0044 | 0.0003 | |
| ITKKVADLVGFLLLK | 15 | 1 n | POL | 102 | 3,11 | | | 0.40 | 1.0 | |
| VTKAEMLESVIKNYK | 15 | 1 n | POL | 123 | 3,11 | | | 0.024 | 0.053 | |
| VVGNWQYFFPVIFSK | 15 | 3 | POL | 79 | 3,11 | | | 1.6 | 0.34 | |
| PRALAETSY | 9 | 1 | new | 268 | 1 | <0.0018 | | <0.0003 | <0.0002 | |
| FATCLGLSY | 9 | 3 | | 171 | 1 | 0.038 | | <0.0003 | 0.0004 | |
| LEQRSLHCK | 9 | 1 | new | 3 | 3 | | | <0.0002 | 0 | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| AEMLESVIK | 9 | 1 | new | 126 | 3 | | | <0.0002 | 0.0011 | |
| LESVIKNYK | 9 | 1 | new | 129 | 3 | | | <0.0002 | 0.0018 | |
| EELSVMEVY | 9 | 1 | new | 216 | 3 | | | <0.0002 | 0 | |
| MEVYDGREH | 9 | 1 | new | 221 | 3 | | | <0.0002 | 0 | |
| DSDPARYEF | 9 | 1 | new | 256 | 3 | | | <0.0002 | 0 | |
| KVSARVRFF | 9 | 1 | new | 285 | 3 | | | 0.0005 | 0 | |
| VSARVRFFF | 9 | 1 | new | 286 | 3 | | | 0.0003 | 0.0026 | |
| HSPQGASSF | 9 | 2 | | 56 | 3 | | | <0.0002 | 0 | |
| TTINYTLWR | 9 | 2 | | 66 | 3 | | | 0.089 | 1.1 | |
| QEEEGPRMF | 9 | 2 | | 83 | 3 | | | <0.0002 | 0 | |
| MFPDLESEF | 9 | 2 | | 90 | 3 | | | <0.0002 | 0 | 0.014 |
| SEFQAAISR | 9 | 2 | | 96 | 3 | | | <0.0002 | 0.0001 | |
| EFQAAISRK | 9 | 2 | | 97 | 3 | | | <0.0002 | 0.0002 | |
| LVHFLLLKY | 9 | 2,3 | | 109 | 3 | | | 0.043 | 0.010 | |
| AEMLESVLR | 9 | 2 | | 126 | 3 | | | <0.0002 | 0 | |
| SVLRNCQDF | 9 | 2 | | 131 | 3 | | | <0.0002 | 0 | |
| VLRNCQDFF | 9 | 2 | | 132 | 3 | | | <0.0002 | 0 | |
| DFFPVIFSK | 9 | 2 | | 138 | 3 | | | <0.0002 | 0.0022 | |
| VIFSKASEY | 9 | 2 | | 142 | 3 | | | 0.081 | 0.033 | |
| VVEVVPISH | 9 | 2 | | 159 | 3 | | | 0.0007 | 0.010 | |
| LGDNQVMPK | 9 | 2 | | 183 | 3 | | | <0.0002 | 0.0061 | |
| EGDCAPEEK | 9 | 2,3 | | 205 | 3 | | | <0.0002 | 0 | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| QEEEGPSTF | 9 | 3 | | 83 | 3 | | | <0.0002 | 0 | |
| TFPDLESEF | 9 | 3 | | 90 | 3 | | | <0.0002 | 0 | 0.0049 |
| SEFQAALSR | 9 | 3 | | 96 | 3 | | | <0.0002 | 0 | |
| EFQAALSRK | 9 | 3 | | 97 | 3 | | | <0.0002 | 0.0001 | |
| SVVGNWQYF | 9 | 3 | | 131 | 3 | | | <0.0002 | 0 | |
| VVGNWQYFF | 9 | 3 | | 132 | 3 | | | 0.0022 | 0.0021 | |
| YFFPVIFSK | 9 | 3 | | 138 | 3 | | | 0.0020 | 0.027 | |
| ASSSLQLVF | 9 | 3 | | 147 | 3 | | | 0.0011 | 0.0089 | |
| LMEVDPIGH | 9 | 3 | | 159 | 3 | | | <0.0002 | 0 | |
| IIVLAIIAR | 9 | 3 | | 196 | 3 | | | 0.0069 | 0.0011 | |
| VQEKYLEYR | 9 | 1 | | 244 | 11 | | | <0.0002 | 0 | |
| SNQEEEGPR | 9 | 2 | | 81 | 11 | | | <0.0002 | 0 | |
| NYKHCFPEI | 9 | 1 | new | 135 | 24 | | | | | 4.8 |
| IFGKASESL | 9 | 1 | new | 143 | 24 | | | | | 0.0013 |
| GFLIIVLVM | 9 | 1 | new | 193 | 24 | | | | | <0.0002 |
| IFSKASEYL | 9 | 2 | | 143 | 24 | | | | | 0.023 |
| EYLQLVFGI | 9 | 2 | | 149 | 24 | | | | | 3.5 |
| NWQYFFPVI | 9 | 3 | | 135 | 24 | | | | | 0.53 |
| IFSKASSSL | 9 | 3 | | 143 | 24 | | | | | 0.016 |
| LGSVVGNWQY | 10 | 3 | | 129 | 1 | <0.0020 | | <0.0003 | 0.0012 | |
| IFATCLGLSY | 10 | 3 | | 170 | 1 | <0.0002 | | 0.0005 | 0.0004 | |
| TSCILESLFR | 10 | 1 | new | 90 | 3 | | | <0.0002 | 0.015 | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| LESVIKNYKH | 10 | 1 | new | 129 | 3 | | | <0.0002 | <0.0002 | |
| REHSAYGEPR | 10 | 1 | new | 227 | 3 | | | <0.0002 | <0.0002 | |
| PDSDPARYEF | 10 | 1 | new | 255 | 3 | | | <0.0002 | <0.0002 | |
| LEYVIKVSAR | 10 | 1 | new | 280 | 3 | | | <0.0002 | <0.0002 | |
| VIKVSARVRF | 10 | 1 | new | 283 | 3 | | | <0.0002 | <0.0002 | |
| KVSARVRFFF | 10 | 1 | new | 285 | 3 | | | 0.0013 | 0.0020 | |
| STTINYTLWR | 10 | 2 | | 65 | 3 | | | 0.0014 | 0.091 | |
| SSNQEEEGPR | 10 | 2 | | 80 | 3 | | | <0.0002 | <0.0002 | |
| RMFPDLESEF | 10 | 2 | | 89 | 3 | | | <0.0002 | <0.0002 | 0.0016 |
| ESEFQAAISR | 10 | 2 | | 95 | 3 | | | <0.0002 | <0.0002 | |
| SEFQAAISRK | 10 | 2 | | 96 | 3 | | | 0.0012 | 0.0028 | |
| ISRKMVELVH | 10 | 2 | | 102 | 3 | | | <0.0002 | <0.0002 | |
| VELVHFLLLK | 10 | 2 | | 107 | 3 | | | 0.0009 | 0.0003 | |
| ELVHFLLLKY | 10 | 2,3 | | 108 | 3 | | | 0.0066 | 0.0003 | |
| LVHFLLLKYR | 10 | 2 | | 109 | 3 | | | 0.026 | 0.0022 | |
| HFLLLKYRAR | 10 | 2,3 | | 111 | 3 | | | 0.0014 | 0.0002 | |
| KAEMLESVLR | 10 | 2 | | 125 | 3 | | | <0.0002 | 0.0009 | |
| ESVLRNCQDF | 10 | 2 | | 130 | 3 | | | <0.0002 | <0.0002 | |
| SVLRNCQDFF | 10 | 2 | | 131 | 3 | | | <0.0002 | <0.0002 | |
| NCQDFFPVIF | 10 | 2 | | 135 | 3 | | | <0.0002 | <0.0002 | |
| QDFFPVIFSK | 10 | 2 | | 137 | 3 | | | <0.0002 | 0.0083 | |
| PVIFSKASEY | 10 | 2 | | 141 | 3 | | | 0.016 | 0.0033 | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| KASEYLQLVF | 10 | 2 | | 146 | 3 | | | <0.0002 | <0.0002 | 0.0030 |
| EVVEVVPISH | 10 | 2 | | 158 | 3 | | | <0.0002 | <0.0002 | |
| VEVVPISHLY | 10 | 2 | | 160 | 3 | | | <0.0002 | <0.0002 | |
| ILVTCLGLSY | 10 | 2 | | 170 | 3 | | | 0.0036 | 0.0002 | |
| LLGDNQVMPK | 10 | 2 | | 182 | 3 | | | 0.0093 | 0.0014 | |
| IEGDCAPEEK | 10 | 2 | | 204 | 3 | | | <0.0002 | <0.0002 | |
| STFPDLESEF | 10 | 3 | | 89 | 3 | | | <0.0002 | <0.0002 | |
| ESEFQAALSR | 10 | 3 | | 95 | 3 | | | <0.0002 | <0.0002 | |
| SEFQAALSRK | 10 | 3 | | 96 | 3 | | | 0.0010 | 0.0010 | |
| LSRKVAELVH | 10 | 3 | | 102 | 3 | | | <0.0002 | <0.0002 | |
| AELVHFLLLK | 10 | 3 | | 107 | 3 | | | 0.0008 | <0.0002 | |
| LVHFLLLKYR | 10 | 3 | | 109 | 3 | | | 0.040 | 0.0014 | |
| GSVVGNWQYF | 10 | 3 | | 130 | 3 | | | 0.0020 | 0.0008 | |
| SVVGNWQYFF | 10 | 3 | | 131 | 3 | | | 0.0085 | 0.0067 | |
| KASSSLQLVF | 10 | 3 | | 146 | 3 | | | 0.0003 | 0.0008 | 0.0021 |
| ELMEVDPIGH | 10 | 3 | | 158 | 3 | | | <0.0003 | <0.0002 | |
| MEVDPIGHLY | 10 | 3 | | 160 | 3 | | | 0.0004 | 0.0004 | |
| VDPIGHLYIF | 10 | 3 | | 162 | 3 | | | <0.0003 | <0.0002 | |
| LIIVLAIIAR | 10 | 3 | | 195 | 3 | | | 0.028 | 0.0021 | |
| REGDCAPEEK | 10 | 3 | | 204 | 3 | | | <0.0003 | <0.0002 | |
| RQPSEGSSSR | 10 | 1 | new | 74 | 11 | | | 0.0009 | 0.0009 | |
| LQLVFGIDVK | 10 | 1 | new | 151 | 11 | | | 0.0050 | 0.0018 | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| RQVPDSDPAR | 10 | 1 | new | 252 | 11 | | | <0.0003 | <0.0002 | |
| MNYPLWSQSY | 10 | 3 | new | 68 | 11 | | | <0.0003 | <0.0002 | |
| GFLIIVLVMI | 10 | 1 | new | 193 | 24 | | | | | 0.0008 |
| SFSTTINYTL | 10 | 2 | | 63 | 24 | | | | | 0.015 |
| EFQAAISRKM | 10 | 2 | | 97 | 24 | | | | | <0.0002 |
| LYILVTCLGL | 10 | 2 | | 168 | 24 | | | | | 0.014 |
| NWQYFFPVIF | 10 | 3 | | 135 | 24 | | | | | 0.017 |
| AVDPIGHLY | 9 | 3 | analog | 161 | 1 | 8.0 | | | | |
| EADPIGHLY | 9 | 3 | analog | 161 | 1 | 3.5 | | | | |
| EVDPASNTY | 9 | 4 | | 161 | 1 | 1.5 | | | | |
| EDTPIGHLY | 9 | 3 | analog | 161 | 1 | 13 | | | | |
| EVDPTGHLY | 9 | 3 | analog | 161 | 1 | 3.0 | | | | |
| AADSPSPPH | 9 | 2 | | 55 | A11 | | | | | |
| VPISHLYIL | 9 | 2 | | 170 | P1 | | | | | |
| MPKTGLLII | 9 | 2 | | 196 | P1 | | | | | |
| SMLEVFEGR | 9 | 2 | | 226 | A11 | | | | | |
| DSVFAHPRK | 9 | 2 | | 236 | A11 | | | | | |
| VFAHPRKLL | 9 | 2 | | 238 | A24 | | | | | |
| MQDLVQENY | 9 | 2 | | 247 | A01 | | | | | |
| DPACYEFLW | 9 | 2 | | 265 | P2 | | | | | |
| FLWGPRALI | 9 | 2 | | 271 | A02 | | | | | |
| ALIETSYVK | 9 | 2 | | 277 | A03/A11 | | | | | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| TSYVKVLHH | 9 | 2 | | 281 | A11 | | | | | |
| EPHISYPPL | 9 | 2 | | 296 | P1 | | | | | |
| ISYPPLHER | 9 | 2 | | 299 | A03/A11 | | | | | |
| YPPLHERAL | 9 | 2 | | 301 | P1 | | | | | |
| EPVTKAEML | 9 | 2/3 | | 128 | P1 | | | | | |
| VPGSDPACY | 9 | 2/3 | | 261 | P2 | | | | | |
| EGLEARGEA | 9 | 3 | | 14 | A03 | | | | | |
| GLEARGEAL | 9 | 3 | | 15 | A02 | | | | | |
| EARGEALGL | 9 | 3 | | 17 | A02 | | | | | |
| ALGLVGAQA | 9 | 3 | | 22 | A02/A03 | | | | | |
| GLVGAQAPA | 9 | 3 | | 24 | A02/A03 | | | | | |
| LVGAQAPAT | 9 | 3 | | 25 | A02 | | | | | |
| PATEEQEAA | 9 | 3 | | 31 | A02/A03 | | | | | |
| EAASSSSTL | 9 | 3 | | 37 | A02 | | | | | |
| AASSSSTLV | 9 | 3 | | 38 | A02 | | | | | |
| LVEVTLGEV | 9 | 3 | | 45 | A02 | | | | | |
| EVTLGEVPA | 9 | 3 | | 47 | A02/A03 | | | | | |
| VTLGEVPAA | 9 | 3 | | 48 | A02/A03 | | | | | |
| LPTTMNYPL | 9 | 3 | | 71 | P1 | | | | | |
| PDLESEFQA | 9 | 3 | | 99 | A03 | | | | | |
| HFLLLKYRA | 9 | 3 | | 118 | A03 | | | | | |
| FFPVIFSKA | 9 | 3 | | 146 | A03 | | | | | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| DPIGHLYIF | 9 | 3 | | 170 | P2 | | | | | |
| GDNQIMPKA | 9 | 3 | | 191 | A03 | | | | | |
| MPKAGLLII | 9 | 3 | | 196 | P1 | | | | | |
| AGLLIIVLA | 9 | 3 | | 199 | A03 | | | | | |
| KIWEELSVL | 9 | 3 | | 220 | A02 | | | | | |
| SVLEVFEGR | 9 | 3 | | 226 | A03/A11 | | | | | |
| EDSILGDPK | 9 | 3 | | 235 | A03/A11 | | | | | |
| SILGDPKKL | 9 | 3 | | 237 | A02 | | | | | |
| ILGDPKKLL | 9 | 3 | | 238 | A02 | | | | | |
| FLWGPRALV | 9 | 3 | | 271 | A02 | | | | | |
| PRALVETSY | 9 | 3 | | 275 | A01 | | | | | |
| RALVETSYV | 9 | 3 | | 276 | A02 | | | | | |
| ALVETSYVK | 9 | 3 | | 277 | A03/A11 | | | | | |
| LVETSYVKV | 9 | 3 | | 278 | A02 | | | | | |
| YVKVLHHMV | 9 | 3 | | 283 | A02 | | | | | |
| KVLHHMVKI | 9 | 3 | | 285 | A02 | | | | | |
| MVKISGGPH | 9 | 3 | | 290 | A03/A11 | | | | | |
| ISGGPHISY | 9 | 3 | | 293 | A01/A03/A11 | | | | | |
| GPHISYPPL | 9 | 3 | | 296 | P1 | | | | | |
| YPPLHEWVL | 9 | 3 | | 301 | P1 | | | | | |
| VPISHLYILV | 10 | 2 | | 170 | P1 | | | | | |
| MPKTGLLIIV | 10 | 2 | | 196 | P1 | | | | | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| VFEGREDSVF | 10 | 2 | | 230 | A24 | | | | | |
| HPRKLLMQDL | 10 | 2 | | 241 | P1 | | | | | |
| LMQDLVQENY | 10 | 2 | | 246 | A01 | | | | | |
| EFLWGPRALI | 10 | 2 | | 270 | A24 | | | | | |
| GPRALIETSY | 10 | 2 | | 274 | P2 | | | | | |
| RALIETSYVK | 10 | 2 | | 276 | A11 | | | | | |
| SYVKVLHHTL | 10 | 2 | | 282 | A24 | | | | | |
| SYPPLHERAL | 10 | 2 | | 300 | A24 | | | | | |
| APEEKIWEEL | 10 | 2/3 | | 216 | P1 | | | | | |
| PLEQRSQHCK | 10 | 3 | | 2 | A03/A11 | | | | | |
| HCKPEEGLEA | 10 | 3 | | 9 | A03 | | | | | |
| EARGEALGLV | 10 | 3 | | 17 | A02 | | | | | |
| RGEALGLVGA | 10 | 3 | | 19 | A03 | | | | | |
| EALGLVGAQA | 10 | 3 | | 21 | A02/A03 | | | | | |
| LGLVGAQAPA | 10 | 3 | | 23 | A03 | | | | | |
| GLVGAQAPAT | 10 | 3 | | 24 | A02 | | | | | |
| QAPATEEQEA | 10 | 3 | | 29 | A02/A03 | | | | | |
| EAASSSSTLV | 10 | 3 | | 37 | A02 | | | | | |
| TLVEVTLGEV | 10 | 3 | | 44 | A02 | | | | | |
| EVTLGEVPAA | 10 | 3 | | 47 | A02/A03 | | | | | |
| PDPPQSPQGA | 10 | 3 | | 59 | A03 | | | | | |
| LPTTMNYPLW | 10 | 3 | | 71 | P2 | | | | | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| PDLESEFQAA | 10 | 3 | | 99 | A03 | | | | | |
| YFFPVIFSKA | 10 | 3 | | 145 | A03 | | | | | |
| LGDNQIMPKA | 10 | 3 | | 190 | A03 | | | | | |
| MPKAGLLIIV | 10 | 3 | | 196 | P1 | | | | | |
| EVFEGREDSI | 10 | 3 | | 229 | A02 | | | | | |
| EDSILGDPKK | 10 | 3 | | 235 | A03/A11 | | | | | |
| SILGDPKKLL | 10 | 3 | | 237 | A02 | | | | | |
| ILGDPKKLLT | 10 | 3 | | 238 | A02 | | | | | |
| GDPKKLLTQH | 10 | 3 | | 240 | A03/A11 | | | | | |
| DPKKLLTQHF | 10 | 3 | | 241 | P2 | | | | | |
| LTQHFVQENY | 10 | 3 | | 246 | A01/A03/A11 | | | | | |
| FVQENYLEYR | 10 | 3 | | 250 | A03/A11 | | | | | |
| ACYEFLWGPR | 10 | 3 | | 267 | A03/A11 | | | | | |
| GPRALVETSY | 10 | 3 | | 274 | P2 | | | | | |
| RALVETSYVK | 10 | 3 | | 276 | A03/A11 | | | | | |
| ALVETSYVKV | 10 | 3 | | 277 | A02 | | | | | |
| LVETSYVKVL | 10 | 3 | | 278 | A02 | | | | | |
| YVKVLHHMVK | 10 | 3 | | 283 | A03/A11 | | | | | |
| MVKISGGPHI | 10 | 3 | | 290 | A02 | | | | | |
| KISGGPHISY | 10 | 3 | | 292 | A01 | | | | | |
| SPPHSPQGA | 9 | 2 | | 60 | P2A | | | | | |
| APATEEQEA | 9 | 3 | | 30 | P2A | | | | | |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| DPPQSPQGA | 9 | 3 | | 60 | P2A | | | | | |
| APATEEQQTA | 10 | 2 | | 30 | P2A | | | | | |
| FPDLESEFQA | 10 | 2/3 | | 98 | P2A | | | | | |
| APATEEQEAA | 10 | 3 | | 30 | P2A | | | | | |
| DPIGHLYIFA | 10 | 3 | | 170 | P2A | | | | | |
| EADPTGHSY | 9 | 1 | | 161 | 1 | 0.56 | 0 | 0 | 0.0002 | <0.0002 |
| KVADLVGFLL | 10 | 1 | | 105 | | 0.0005 | 0.041 | 0.0039 | 0.0030 | 0.0070 |
| ASSLPTTMNY | 10 | 3 | | 8 | 1 | 2.3 | | | 0.043 | |
| TQDLVQEKY | 9 | 1 | | 240 | 1 | 0.57 | 0.0001 | 0 | 0 | 0 |
| LVQEKYLEY | 9 | 1 | | 243 | 3 | 016 | 0 | 0.0016 | 0.0098 | 0 |
| ILLWQPIPV | 9 | 3 | | | | <0.0007 | 1.4 | 0.0048 | 0.0048 | 0 |
| EVDPIGHLY | 9 | 3 | | | | 3.7 | | | 0.0022 | |
| ASSFSTTINY | 10 | 2 | | 8 | 1 | 0.016 | 0 | 0.0016 | 0.0054 | 0 |
| VTCLGLSY | 8 | 1 | | 172 | 1 | 0.022 | 0 | 0.0001 | 0.0007 | 0 |
| SSLPTTMNY | 9 | 3 | | 9 | 1 | 0.037 | 0 | 0.013 | 0.12 | 0 |
| GSVVGNWQY | 9 | 3 | | 77 | 1 | 0.0059 | 0 | 0.0009 | 0.025 | 0 |
| DLVQEKYLEY | 10 | 1 | new | 242 | 3 | 0 | 0 | 0.0010 | 0 | 0 |
| SSFSTTINY | 9 | 2 | | 9 | 1 | 0.016 | 0 | 0.0095 | 0.056 | 0 |
| MLESVIKNY | 9 | 1 | | 128 | 1 | 0.0016 | 0.0002 | 0.0006 | 0 | 0 |
| KMVELVHFL | 9 | 2 | | | | <0.0007 | 0.13 | 0.0007 | 0 | 0.0043 |
| KMVELVHFLL | 10 | 2 | | 105 | | <0.0008 | 0.071 | 0.0004 | 0.0001 | 0.0008 |
| LVFGIELMEV | 10 | 3 | | | | 0.0030 | 0.065 | 0.0007 | 0 | 0 |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| SLFRAVITK | 9 | 1 | | 96 | 3,11 | <0.0007 | 0.0001 | 3.9 | 2.6 | 0 |
| ADLVGFLLLK | 10 | 1 | | 107 | 3 | 0.0012 | 0.0003 | 0.0081 | 0.022 | 0 |
| ESLFRAVITK | 10 | 1 | | 95 | 3 | <0.0008 | 0 | 0.0090 | 0.0052 | 0 |
| MLESVIKNYK | 10 | 1 | | | | 0 | 0 | 0.034 | 0.0045 | 0 |
| LVGFLLLK | 8 | 1 | | 109 | 3 | 0.0029 | 0.0002 | 0.027 | 0.034 | 0 |
| TTINFTRQR | 9 | 1 | | 66 | 3,11 | 0 | 0 | 0.051 | 0.40 | 0 |
| LLGDNQIMPK | 10 | 1/3 | | 182 | 3,11 | <0.0007 | 0.0001 | 0.022 | 0.016 | 0 |
| SVMEVYDGR | 9 | 1 | | 219 | 3,11 | <0.0006 | 0 | 0.059 | 0.32 | 0 |
| HSAYGEPRK | 9 | 1 | | 229 | 3 | 0.0007 | 0 | 0.0070 | 0.0015 | 0 |
| LLTQDLVQEK | 10 | 1 | | 238 | 3,11 | <0.0007 | 0 | 0.0014 | 0.011 | 0 |
| LTQDLVQEK | 9 | 1 | | 239 | 3,11 | 0.0011 | 0 | 0.0002 | 0.16 | 0 |
| NYKHCFPEIF | 10 | 1 | | 135 | 24 | 0 | 0 | 0 | 0 | 0.26 |
| LYIFATCLGL | 10 | 3 | | 115 | 24 | <0.0007 | 0 | 0.0006 | 0 | 0.0035 |
| NYPLWSQSY | 9 | 3 | | 16 | 24 | <0.0006 | 0 | 0 | 0.0001 | 0.016 |
| SYVLVTCL | 8 | 1 | | 168 | 24 | 0.0029 | 0.00025 | 0.0020 | 0.0002 | 0.0026 |
| ETSYVKVLEY | 10 | 1 | | | | 0.075 | 0 | 0.0009 | 0.0004 | 0 |
| TSYVKVLEY | 9 | 1 | | 275 | 3 | 0.082 | 0 | 0.23 | 0.013 | 0 |
| FLWGPRALA | 9 | 1 | | | | <0.0006 | 0.027 | 0.0015 | 0 | 0 |
| ALAETSYVKV | 10 | 1 | | 271 | | <0.0007 | 0.017 | 0.0011 | 0.0029 | 0 |
| RVRFFFPSLR | 10 | 1 | | 290 | 3 | <0.0007 | 0 | 0.25 | 0.0035 | 0 |
| ALAETSYVK | 9 | 1 | | | | <0.0006 | 0.0002 | 0.17 | 0.39 | 0 |
| LTQDLVQEKY | 10 | 1 | | 239 | 1 | 0.041 | 0 | 0 | 0.0002 | 0 |

Table 5

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| GFLLLKYRA | 9 | 1 | | | | | | 0.0004 | 0.0002 | |
| CFPEIFGKA | 9 | 1 | | | | | | 0 | 0 | |
| FFFPSLREA | 9 | 1 | | | | | | 0 | 0 | |
| FFPSLREAA | 9 | 1 | | | | | | 0 | 0 | |
| HCFPEIFGK | 9 | 1 | | 138 | 3,11 | | | 0.0017 | 0.0022 | |
| RSLHCKPEEA | 10 | 1 | | | | | | 0.0001 | 0.0008 | |
| EFLWGPRALA | 10 | 1 | | | | | | 0 | 0 | |
| RFFFPSLREA | 10 | 1 | | | | | | 0.0004 | 0 | |
| FFFPSLREAA | 10 | 1 | | | | | | 0 | 0 | |

Table 5

| Sequence | Antigen | Strain | Molecule | Position | Motif | A1 Binding | A2 Binding | A3 Binding | A11 Binding | A24 Binding | Max. Binding |
|---|---|---|---|---|---|---|---|---|---|---|---|
| FSPAFDNLYY | c-ErbB2 | | | 1213 | A01 | 5.5000 | | 0.0005 | 0.0010 | | 5.5000 |
| CMQIAKGMSY | c-ErbB2 | | | 826 | A01 | 0.2967 | | 0.0003 | 0.0001 | | 0.2967 |
| ESMPNPEGRY | c-ErbB2 | | | 280 | A01 | 0.1800 | | 0.0003 | 0.0003 | | 0.1800 |
| ASCVTACPY | c-ErbB2 | | | 293 | A01 | 0.0552 | | 0.0008 | 0.0074 | | 0.0552 |
| FSPAFDNLY | c-ErbB2 | | | 1213 | A01 | 0.0425 | | 0.0002 | 0.0002 | | 0.0425 |
| ASPLDSTFY | c-ErbB2 | | | 997 | A01 | 0.0290 | | 0.0002 | 0.0004 | | 0.0290 |
| RGTQLFEDNY | c-ErbB2 | | | 103 | A01 | 0.0205 | | 0.0003 | 0.0015 | | 0.0205 |
| PASPLDSTFY | c-ErbB2 | | | 996 | A01 | 0.0148 | | 0.0003 | 0.0001 | | 0.0148 |
| LSAFSLHSY | HCV | | | 2889 | A01 | 0.8100 | | 0.0002 | 0.0002 | | 0.8100 |
| KSTKVPAAY | HCV | | | 1236 | A01 | 0.0134 | | 0.0009 | 0.0001 | | 0.0134 |
| DSSVLCECY | HCV | | | 1513 | A01 | 0.0110 | | 0.0002 | 0.0003 | | 0.0110 |
| ETDPIGHLY | MAGE-3a | 3 | analog | 161 | A01 | 12.5000 | | | | | 12.5000 |
| AVDPIGHLY | MAGE-3a | 3 | analog | 161 | A01 | 8.0000 | | | | | 8.0000 |
| EVDPIAHLY | MAGE-3a | 3 | analog | 161 | A01 | 5.5000 | | | | | 5.5000 |
| EVDAIGHLY | MAGE-3a | 3 | analog | 161 | A01 | 5.3500 | | | | | 5.3500 |
| EVDPIGALY | MAGE-3a | 3 | analog | 161 | A01 | 5.0000 | | | | | 5.0000 |
| EVDPIGHAY | MAGE-3a | 3 | analog | 161 | A01 | 4.6500 | | | | | 4.6500 |
| EADPIGHLY | MAGE-3a | 3 | analog | 161 | A01 | 3.4500 | | | | | 3.4500 |
| EVDPTGHLY | MAGE-3a | 3 | analog | 161 | A01 | 2.9500 | | | | | 2.9500 |
| EVDPIGHSY | MAGE-3a | 3 | analog | 161 | A01 | 2.6667 | | | | | 2.6667 |
| EVDPAGHLY | MAGE-3a | 3 | analog | 161 | A01 | 2.4000 | | | | | 2.4000 |
| EVDPIGHLA | MAGE-3a | 3 | analog | 161 | A01 | 0.3300 | | | | | 0.3300 |
| EVAPIGHLY | MAGE-3a | 3 | analog | 161 | A01 | 0.1800 | | | | | 0.1800 |
| EVDPASNTY | MAGE-4 | 4 | | 161 | A01 | 1.5000 | | | | | 1.5000 |
| VGSDCTTIHY | p53 | | | 225 | A01 | 0.2600 | | 0.0003 | 0.0003 | | 0.2600 |
| PSQKTYQGSY | p53 | | | 98 | A01 | 0.0140 | | 0.0003 | 0.0003 | | 0.0140 |
| PLSEDQLLY | PAP | | | 147 | A01 | 1.2000 | | 0.0005 | 0.0001 | | 1.2000 |
| IPSYKKLIMY | PAP | | | 277 | A01 | 0.5650 | | | | | 0.5650 |
| YASCHLTELY | PAP | | | 310 | A01 | 0.5467 | | 0.0003 | 0.0002 | | 0.5467 |

Table 5

| Sequence | Antigen | Strain | Molecule | Position | Motif | A1 Binding | A2 Binding | A3 Binding | A11 Binding | A24 Binding | Max. Binding |
|---|---|---|---|---|---|---|---|---|---|---|---|
| RVLQGLPREY | c-ERB2 | | | 545 | A03 | 0.0015 | | 0.0350 | 0.0050 | | 0.0350 |
| QLVTQLMPY | c-ERB2 | | | 795 | A03 | 0.0024 | | 0.0112 | 0.0039 | | 0.0112 |
| VMAGVGSPY | c-ErbB2 | | | 773 | A03 | 0.0400 | | 0.0575 | 0.0079 | | 0.0575 |
| TLWKAGILY | HBV | adr | POL | 724 | A03 | 0.0017 | | 0.2667 | 0.0016 | | 0.2667 |
| ILRGTSFVY | HBV | adr | POL | 1345 | A03 | 0.0017 | | 0.0440 | 0.0002 | | 0.0440 |
| KLNWASQIY | HIV | | POL | 958 | A03 | 0.0070 | | 0.1160 | 0.0006 | | 0.1160 |
| GLNKIVRMY | HIV | | GAG | 274 | A03 | 0.0017 | | 0.0103 | 0.0002 | | 0.0103 |
| LVGFLLLKY | MAGE-1 | 1 | | 109 | A03 | 0.0033 | | 0.0563 | 0.0012 | | 0.0563 |
| GTRVRAMAIY | p53 | | | 154 | A03 | 0.0027 | | 0.0365 | 0.0002 | | 0.0365 |
| KIQNFRVYY | HIV | | POL | 1474 | A03/A11 | 0.0056 | | 0.1190 | 0.1350 | | 0.1350 |
| SLYTKVVHY | PSA | | | 237 | A03/A11 | 0.0017 | | 0.6750 | 0.0140 | | 0.6750 |
| LTCGFADIMGY | HCV | | | 126 | A11 | 2.4500 | | 0.0003 | 0.0120 | 0.0001 | 2.4500 |
| ETAYFLLK | HIV | con | | 1351 | A11 | | | 0.0037 | 0.0425 | | 0.0425 |
| RWGLLLALL | c-ErbB2 | | | 8 | A24 | | | | | 1.2567 | 1.2567 |
| PYVSRLLGI | c-ErbB2 | | | 780 | A24 | | | | | 0.1650 | 0.1650 |
| VYMIMVKCW | c-ErbB2 | | | 951 | A24 | | | | | 0.1640 | 0.1640 |
| AYSLTLQGL | c-ErbB2 | | | 440 | A24 | | | | | 0.1250 | 0.1250 |
| SYGVTVWEL | c-ErbB2 | | | 907 | A24 | | | | | 0.1200 | 0.1200 |
| LYISAWPDSL | c-ErbB2 | | | 410 | A24 | | | | | 0.0835 | 0.0835 |
| VWSYGVTVW | c-ErbB2 | | | 905 | A24 | | | | | 0.0800 | 0.0800 |
| SYGVTVWELM | c-ErbB2 | | | 907 | A24 | | | | | 0.0630 | 0.0630 |
| TYLPTNASL | c-ErbB2 | | | 63 | A24 | | | | | 0.0375 | 0.0375 |
| VYMIMVKCWM | c-ErbB2 | | | 951 | A24 | | | | | 0.0218 | 0.0218 |
| RFRELVSEF | c-ErbB2 | | | 968 | A24 | | | | | 0.0180 | 0.0180 |
| CYGLGMEHL | c-ErbB2 | | | 342 | A24 | | | | | 0.0176 | 0.0176 |
| KWMALESIL | c-ErbB2 | | | 887 | A24 | | | | | 0.0149 | 0.0149 |
| EYLVPQQGFF | c-ErbB2 | | | 1022 | A24 | | | | | 0.0120 | 0.0120 |
| RYSEDPTVPL | c-ErbB2 | | | 1111 | A24 | | | | | 0.0117 | 0.0117 |
| RFTHQSDVW | c-ErbB2 | | | 898 | A24 | | | | | 0.0107 | 0.0107 |

Table 5

| Sequence | Antigen | Strain | Molecule | Position | Motif | A1 Binding | A2 Binding | A3 Binding | A11 Binding | A24 Binding | Max. Binding |
|---|---|---|---|---|---|---|---|---|---|---|---|
| EYLVSFGVWI | HBV | | NUC | 117 | A24 | | | | | 0.0335 | 0.0335 |
| WFHISCLTF | HBV | | NUC | 102 | A24 | | | | | 0.0300 | 0.0300 |
| QYLAGLSTL | HCV | | | 1777 | A24 | | | | | 0.0475 | 0.0475 |
| TYSTYGKFL | HCV | | | 1296 | A24 | | | | | 0.0225 | 0.0225 |
| QYSPGQRVEF | HCV | | | 2614 | A24 | | | | | 0.0175 | 0.0175 |
| KFMLCAGRW | PSA | | | 190 | A24 | | 0.0003 | | | 0.0305 | 0.0305 |

Table 6

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | GLNKIVRMY | HIV GAG 274 |
| 9 | KLNWASQIY | HIV POL 958 |
| 9 | KIQNFRVYY | HIV POL 1474 |
| 9 | TLWKAGILY | HBV adr POL 724 |
| 9 | ILRGTSFVY | HBV adr POL 1345 |
| 9 | SLYTKVVHY | PSA 237 |
| 9 | NTSSSPQPK | p53 311 |
| 9 | NVKIPVAIK | c-ERB2 745 |
| 10 | TLGFGAYMSK | HCV LORF 1261 |
| 10 | GTRVRAMAIY | p53 154 |
| 10 | EAYSPVSTSK | HBV adw POL 887 |
| 9 | QITKIQNFR | HIV POL 1471 |
| 9 | NITGLILTR | HIV ENV 2633 |
| 9 | FLWEWASVR | HBV adr ENV 324 |
| 9 | RTPSPRRRR | HBV adr CORE 549 |
| 9 | SLARGNQGR | HBV adr POL 805 |
| 10 | VAYQATVCAR | HCV LORF 1587 |
| 10 | KTYQGSYGFR | p53 101 |
| 9 | WMCLRRFII | HBV ayw 237 |
| 9 | WMCLRRFII | HBV ayw 237-245 |
| 9 | KFMLCAGRW | PSA 190 |
| 10 | IMPKTGFLII | MAGE 1 188 |
| 8 | ETAYFLLK | HIV con 1351 |
| 11 | LTCGFADIMGY | HCV 126 |
| 9 | CSPHHTALR | HBV NUC;XNUCFUS 48 |
| 9 | VMPKTGLLI | MAGE 2 188 |
| 9 | VMPKTGLLI | MAGE2 188-196 |
| 9 | VAELVHFLL | MAGE 3 106 |
| 9 | IMPKAGLLI | MAGE 3 188 |
| 10 | VMPKTGLLII | MAGE 2 188 |
| 10 | VMPKTGLLII | MAGE2 188-197 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | ASCVTACPY | c-ErbB2 293 |
| 9 | VMAGVGSPY | c-ErbB2 773 |
| 9 | ASPLDSTFY | c-ErbB2 997 |
| 9 | FSPAFDNLY | c-ErbB2 1213 |
| 9 | KSTKVPAAY | HCV 1236 |
| 9 | DSSVLCECY | HCV 1513 |
| 9 | LSAFSLHSY | HCV 2889 |
| 9 | PLSEDQLLY | PAP 147 |
| 9 | YAVCDKCLK | HPV 16 E6 67 |
| 9 | CMSCCRSSR | HPV 16 E6 143 |
| 9 | RWGLLLALL | c-ErbB2 8 |
| 9 | TYLPTNASL | c-ErbB2 63 |
| 9 | CYGLGMEHL | c-ErbB2 342 |
| 9 | AYSLTLQGL | c-ErbB2 440 |
| 9 | PYVSRLLGI | c-ErbB2 780 |
| 9 | KWMALESIL | c-ErbB2 887 |
| 9 | RFTHQSDVW | c-ErbB2 898 |
| 9 | VWSYGVTVW | c-ErbB2 905 |
| 9 | SYGVTVWEL | c-ErbB2 907 |
| 9 | VYMIMVKCW | c-ErbB2 951 |
| 9 | RFRELVSEF | c-ErbB2 968 |
| 9 | WFHISCLTF | HBV NUC 102 |
| 9 | TYSTYGKFL | HCV 1296 |
| 9 | QYLAGLSTL | HCV 1777 |
| 10 | IPSYKKLIMY | PAP 277 |
| 10 | RGTQLFEDNY | c-ErbB2 103 |
| 10 | ESMPNPEGRY | c-ErbB2 280 |
| 10 | CMQIAKGMSY | c-ErbB2 826 |
| 10 | PASPLDSTFY | c-ErbB2 996 |
| 10 | FSPAFDNLYY | c-ErbB2 1213 |
| 10 | PSQKTYQGSY | p53 98 |
| 10 | VGSDCTTIHY | p53 225 |
| 10 | YASCHLTELY | PAP 310 |
| 10 | LYISAWPDSL | c-ErbB2 410 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | SYGVTVWELM | c-ErbB2 907 |
| 10 | VYMIMVKCWM | c-ErbB2 951 |
| 10 | EYLVPQQGFF | c-ErbB2 1022 |
| 10 | RYSEDPTVPL | c-ErbB2 1111 |
| 10 | EYLVSFGVWI | HBV NUC 117 |
| 10 | QYSPGQRVEF | HCV 2614 |
| 9 | VYNFATCGI | LCMV glyco 35 |
| 9 | GYCLTKWMI | LCMV glyco 283 |
| 9 | MFEALPHII | LCMV glyco 7 |
| 9 | IFALISFLL | LCMV glyco 43 |
| 9 | LFKTTVNSL | LCMV glyco 342 |
| 9 | LYTVKYPNL | LCMV nucleo 204 |
| 9 | PYIACRTSI | LCMV nucleo 314 |
| 10 | GYCLTKWMIL | LCMV glyco 283 |
| 10 | AYLVSIFLHL | LCMV glyco 446 |
| 9 | RWCIPWQRL | CEA 10 |
| 9 | IYPNASLLI | CEA 101 |
| 9 | LWWVNNQSL | CEA 177 |
| 9 | LYGPDAPTI | CEA 234 |
| 9 | VYAEPPKPF | CEA 318 |
| 9 | LWWVNNQSL | CEA 355 |
| 9 | LYGPDDPTI | CEA 412 |
| 9 | TYYRPGVNL | CEA 425 |
| 9 | LYGPDTPII | CEA 590 |
| 9 | QYSWRINGI | CEA 624 |
| 9 | TYACFVSNL | CEA 652 |
| 9 | VWKTWGQYW | gp100 152 |
| 9 | TWGQYWQFL | gp100 155 |
| 9 | RYGSFSVTL | gp100 479 |
| 9 | LMAVVLASL | gp100 606 |
| 9 | HWLRLPRIF | gp100 636 |
| 9 | SYKHEQVYI | PAP 96 |
| 9 | AMTNLAALF | PAP 116 |
| 9 | VFLTLSVTW | PSA 2 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | TWIGAAPLI | PSA 9 |
| 9 | CYASGWGSI | PSA 148 |
| 10 | YMIMVKCWMI | c-ErbB2 952 |
| 10 | RWCIPWQRLL | CEA 10 |
| 10 | FWNPPTTAKL | CEA 27 |
| 10 | QYSWFVNGTF | CEA 268 |
| 10 | TFQQSTQELF | CEA 276 |
| 10 | VYAEPPKPFI | CEA 318 |
| 10 | YYRPGVNLSL | CEA 426 |
| 10 | QYSWLIDGNI | CEA 446 |
| 10 | SYLSGANLNL | CEA 604 |
| 10 | HFLRNQPLTF | gp100 231 |
| 10 | LFPPEGVSIW | PAP 123 |
| 10 | TWIGAAPLIL | PSA 9 |
| 10 | HYRKWIKDTI | PSA 244 |
| 9 | KLRKPKHKK | P. falciparum CSP 104 |
| 9 | KILSVFFLA | P. falciparum EXP-1 2 |
| 9 | ALFFIIFNK | P. falciparum EXP-1 10 |
| 9 | GTGSGVSSK | P. falciparum EXP-1 28 |
| 9 | VLYNTEKGR | P. falciparum EXP-1 99 |
| 9 | KYKLATSVL | P. falciparum EXP-1 73 |
| 9 | PSENERGYY | P. falciparum LSA1 1664 |
| 9 | FLKENKLNK | P. falciparum LSA1 111 |
| 9 | GVSENIFLK | P. falciparum LSA1 105 |
| 9 | ILVNLLIFH | P. falciparum LSA1 12 |
| 9 | KSLYDEHIK | P. falciparum LSA1 1854 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | LLIFHINGK | P. falciparum LSA1 16 |
| 9 | QSSLPQDNR | P. falciparum LSA1 1676 |
| 9 | QTNFKSLLR | P. falciparum LSA1 94 |
| 9 | RINEEKHEK | P. falciparum LSA1 49 |
| 9 | SLYDEHIKK | P. falciparum LSA1 1855 |
| 9 | VLAEDLYGR | P. falciparum LSA1 1647 |
| 9 | VLSHNSYEK | P. falciparum LSA1 60 |
| 9 | FYFILVNLL | P. falciparum LSA1 9 |
| 9 | YYIPHQSSL | P. falciparum LSA1 1671 |
| 9 | PSDGKCNLY | P. falciparum TRAP 207 |
| 9 | LACAGLAYK | P. falciparum TRAP 511 |
| 9 | LLACAGLAY | P. falciparum TRAP 510 |
| 9 | LSTNLPYGR | P. falciparum TRAP 122 |
| 9 | QGINVAFNR | P. falciparum TRAP 192 |
| 9 | RGDNFAVEK | P. falciparum TRAP 307 |
| 9 | RSRKREILH | P. falciparum TRAP 262 |
| 9 | SLLSTNLPY | P. falciparum TRAP 120 |
| 9 | KYLVIVFLI | P. falciparum TRAP 8 |
| 9 | PYAGEPAPF | P. falciparum TRAP 528 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | VTCGNGIQVR | P. falciparum CSP 375 |
| 10 | GTGSGVSSKK | P. falciparum EXP-1 28 |
| 10 | LALFFIIFNK | P. falciparum EXP-1 9 |
| 10 | FQDEENIGIY | P. falciparum LSA1 1794 |
| 10 | FILVNLLIFH | P. falciparum LSA1 11 |
| 10 | HVLSHNSYEK | P. falciparum LSA1 59 |
| 10 | KSLYDEHIKK | P. falciparum LSA1 1854 |
| 10 | ALLACAGLAY | P. falciparum TRAP 509 |
| 10 | IIRLHSDASK | P. falciparum TRAP 100 |
| 10 | LLACAGLAYK | P. falciparum TRAP 510 |
| 10 | RLHSDASKNK | P. falciparum TRAP 102 |
| 9 | ILGFVFTLT-NH2 | Flu Matrix 59-67 |
| 10 | KGILGFVFTL-NH2 | Flu Matrix 57-66 |
| 9 | KLQCVPLHV | PSA 166-174 P/D |
| 9 | KLQCVPLHV | PSA 166-174 P/D |
| 9 | KLQCVPLHV | PSA 166-174 P/D |
| 11 | KQVPLRPMTYK | 940.03 N-terminal extension |
| 9 | KLYEIVAKV | A2.1 consensus |
| 9 | KLAEYVAKV | A2.1 consensus |
| 9 | KLAEIVYKV | A2.1 consensus |
| 9 | KVFEYLINK | A3.2 consensus |
| 10 | KVFPYALINK | A3.2 consensus |
| 9 | AVFAYAAAK | A3.2 consensus |
| 9 | ALEPAIAKY | A1 consensus |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | YLEPAIAKY | A1 consensus |
| 9 | ALEPYIAKY | A1 consensus |
| 9 | YLEQYIEKY | A1 consensus |
| 9 | GTEKLLAKY | A1 consensus |
| 9 | ATEPAIAKY | A1 consensus |
| 9 | ATNYPAIQK | A11 consensus |
| 9 | ATNVPAIQK | A11 consensus |
| 9 | ATNAPYIQK | A11 consensus |
| 9 | ATNAVYIQK | A11 consensus |
| 9 | ATNAAYAQK | A11 consensus |
| 9 | AVNAAYAQK | A11 consensus |
| 9 | AVNAPYIQK | A11 consensus |
| 9 | AVNAVYIQK | A11 consensus |
| 9 | PTDPKLINY | A1 consensus |
| 9 | GTDPKLINY | A1 consensus |
| 9 | YTDPKLINF | A1 consensus |
| 9 | FTDPKLINY | A1 consensus |
| 9 | FTDQAVIKY | A1 consensus |
| 9 | YTDQAVIKF | A1 consensus |
| 9 | YTDQKLINF | A1 consensus |
| 9 | STNPKPQKK | HCV-core 2-10 |
| 11 | STNPKPQKKNK | HCV-core 2-12 |
| 9 | SFFPEITYI | self peptide of P815 analog; Y2 to F, |
| 9 | ATDPNFLLY | A1 consensus |
| 9 | ATDKNFLLY | A1 consensus |
| 9 | ALMEKIYQV | A2.1 consensus peptide |
| 9 | ALSEKIYQV | A2.1 consensus peptide |
| 9 | AVYDPIIQK | A3.2 consensus peptide |
| 9 | AVYDKIIQK | A3.2 consensus peptide |
| 9 | AVMNPMIQK | A11 consensus peptide |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | AVMNEMIQK | A11 consensus peptide |
| 9 | AYMDMVNSF | A24 consensus peptide |
| 9 | AYIDNVNSF | A24 consensus peptide |
| 9 | KLAAAAAAK | A3.2/A11 poly-A analog |
| 9 | DVFRDPALK | Aw68 endogenous |
| 9 | GYKDGNEYI | Lm listeriolysin 91-99 |
| 10 | MMWYWGPSLY | HBV |
| 11 | WMMWYWGPSLY | HBV |
| 9 | RYLRDQQLL | HIV env |
| 8 | FLLLKYRA | MAGE-1 |
| 9 | IMPKTGFLI | MAGE-1 |
| 9 | VADLVGFLL | MAGE-1 |
| 10 | IMPKTGFLII | MAGE-1 |
| 11 | FLIIVLVMIAM | MAGE-1 |
| 11 | CILESCFRAVI | MAGE-1 |
| 9 | MYRPDAIQL | P. Yoelii SSP2 143 |
| 10 | NYSPNGNTNL | P. Yoelii SSP2 119 |
| 9 | KFNPMKTHI | Kd consensus peptide |
| 9 | AMIKNLDFI | Db consensus |
| 9 | AMIKNLYFI | Db consensus analog |
| 11 | STLPETYVVRR | HCV 141-151 analog |
| 9 | QYDDAVYKL | Cw4 consensus |
| 10 | FQDPQERPRK | HPV16 E6 |
| 10 | VFEFAFKDLF | HPV18 E6 |
| 9 | VVYRDSIPH | HPV18 E6 |
| 9 | IFEANGNLI | Flu HA 240-248 |
| 9 | IYATVAGSL | HA 529-537 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | SYIPSAEKI | P. bergaii CS 252-260 |
| 9 | KYQAVTTTL | Tumour P198 14-22 |
| 10 | MYPHFMPTNL | MCMV pp89 167-176 |
| 9 | AYPNVSAKI | Lm listeriolysin 196-204 |
| 9 | AYTGGKINI | Lm listeriolysin 413-421 |
| 9 | SAISSILSK | HBV ENV 159 |
| 9 | QAGFFLLTK | HBV ENV 190 |
| 9 | SALYREALK | HBV NUC 64 |
| 9 | RAKWNNTLK | HIV env 370 |
| 9 | RATQIPSYK | PAP 273 |
| 9 | TAAHCIRNK | PSA 58 |
| 9 | MAVFIHNFK | HIV pol 909 |
| 9 | TAGILELLK | HPV 6b E1 192 |
| 9 | RAALLGKFK | HPV 6b E1 205 |
| 9 | CATMCRHYK | HPV 6b E1 406 |
| 9 | TAACSHEGK | Flu HA-1 132 |
| 9 | NANANSAVK | P. fal csp 304 |
| 9 | GAFKVPGVK | LCMV glyco 484 |
| 9 | RARVHPTTR | HBV POL 244 |
| 9 | CALPFTSAR | HBV X 69 |
| 9 | NMLESILIK | LCMV nuc 259 |
| 9 | WMILAAELK | LCMV glyco 289 |
| 9 | EMNLPGRWK | HIV pol 107 |
| 9 | SSLQSKHRK | HBV POL 201 |
| 9 | GSTHVSWPK | HBV POL 398 |
| 9 | TSDLEAYFK | HBV X NUC FUS 105 |
| 9 | ASQIYAGIK | HIV pol 438 |
| 9 | ASCDKCQLK | HIV pol 769 |
| 9 | MSLAADLEK | LCMV nuc 100 |
| 9 | VSSKNLMEK | Mel. tyro 25 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | LSTNLPYGK | P. fal ssp2 122 |
| 9 | STDHIPILY | A1 Nat. Processed |
| 9 | STAPPAHGV | Breast mucin 9-17 |
| 9 | LMAVVLASL | gp100 |
| 9 | WSQKRSFVY | gp100 |
| 9 | PLDCVLYRY | gp100 |
| 10 | PSSVGSRSEY | gp100 |
| 9 | YTAVVPLVY | Hu J chain 102-110 |

Table 7

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 8 | LTELYFEK | PAP 315 |
| 9 | TISPSYTYY | CEA 419 |
| 9 | GTGCNGWFY | HPV 16/18 E1 11 |
| 9 | LTEMVQWAY | HPV 6b/11 E1 358 |
| 9 | ITVNNSGSY | CEA 289 |
| 9 | CTGWFMVEA | HPV 6b/11 E1 14 |
| 9 | ATVQDLKRK | HPV 6b/11 E1 77 |
| 9 | AVESEISPR | HPV 6b/11 E1 101 |
| 9 | FLNSNMQAK | HPV 6b/11 E1 393 |
| 9 | ITRQTVIEH | HPV 6b/11 E1 341 |
| 9 | IVGPPDTGK | HPV 6b/11 E1 476 |
| 9 | KLIEPLSLY | HPV 6b/11 E1 254 |
| 9 | KLWLHGTPK | HPV 6b/11 E1 462 |
| 9 | KMSIKQWIK | HPV 6b/11 E1 420 |
| 9 | VVAGFGIHH | HPV 6b/11 E1 238 |
| 9 | HLFGYSWYK | CEA 61 |
| 9 | ISPSYTYYR | CEA 420 |
| 9 | HTQVLFIAK | CEA 636 |
| 9 | ITVYAEPPK | CEA 316 |
| 9 | ITVSAELPK | CEA 494 |
| 9 | RLQLSNGNR | CEA 190 |
| 9 | RLQLSNGNR | CEA 546 |
| 9 | RINGIPQQH | CEA 628 |
| 9 | SNMQAKYVK | HPV 6b/11 E1 396 |
| 9 | EWITRQTVI | HPV 6b/11 E1 339 |
| 9 | FFERLSSSL | HPV 6b/11 E1 613 |
| 9 | NWKPIVQFL | HPV 6b/11 E1 439 |
| 10 | PTISPSYTYY | CEA 418 |
| 10 | PTISPLNTSY | CEA 240 |
| 10 | HSASNPSPQY | CEA 616 |
| 10 | KLIEPLSLYA | HPV 6b/11 E1 254 |
| 10 | AIVGPPDTGK | HPV 6b/11 E1 475 |
| 10 | DCATMCRHYK | HPV 6b/16 E1 405 |
| 10 | KLWLHGTPKK | HPV 6b/11 E1 462 |
| 10 | WVVAGFGIHH | HPV 6b/11 E1 237 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | TITVSAELPK | CEA 493 |
| 10 | TFWNPPTTAK | CEA 26 |
| 10 | TISPSYTYYR | CEA 419 |
| 10 | TISPLNTSYR | CEA 241 |
| 10 | RTLTLFNVTR | CEA 198 |
| 10 | RTLTLFNVTR | CEA 554 |
| 10 | RTLTLLSVTR | CEA 376 |
| 10 | ATPGPAYSGR | CEA 89 |
| 10 | ASGHSRTTVK | CEA 483 |
| 10 | QFLRHQNIEF | HPV 6b/11 E1 445 |
| 10 | TFTFPNPFPF | HPV 6b/11 E1 586 |
| 9 | RVDCTPLMY | Prost.Ca PSM 463 |
| 9 | LLSLYGIHK | Prost.Ca PAP 243 |
| 9 | SIVLPFDCR | Prost.Ca PSM 590 |
| 9 | KSLYESWTK | Prost.Ca PSM 491 |
| 9 | SMKHPQEMK | Prost.Ca PSM 615 |
| 9 | SLYESWTKK | Prost.Ca PSM 492 |
| 9 | YSLVHNLTK | Prost.Ca PSM 471 |
| 9 | HLTELYFEK | Prost.Ca PAP 314 |
| 9 | RATQIPSYK | Prost.Ca PAP 273 |
| 9 | ASGRARYTK | Prost.Ca PSM 531 |
| 9 | SLYGIHKQK | Prost.Ca PAP 245 |
| 9 | RDYAVVLRK | Prost.Ca PSM 598 |
| 9 | SSHDLMLLR | Prost.Ca PSA 113 |
| 9 | GAAPLILSR | Prost.Ca PSA 12 |
| 9 | KIVIARYGK | Prost.Ca PSM 199 |
| 9 | RAAPLLLAR | Prost.Ca PAP 2 |
| 9 | VVLRKYADK | Prost.Ca PSM 602 |
| 9 | GLPDRPFYR | Prost.Ca PSM 680 |
| 9 | WLDRSVLAK | Prost.Ca PAP 25 |
| 9 | KVFRGNKVK | Prost.Ca PSM 207 |
| 9 | IVRSFGTLK | Prost.Ca PSM 398 |
| 9 | KIYSISMKH | Prost.Ca PSM 610 |
| 9 | RSVLAKELK | Prost.Ca PAP 28 |
| 9 | STNEVTRIY | Prost.Ca PSM 348 |
| 9 | GFFLLGFLF | Prost.Ca PSM 31 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | LYSDPADYF | Prost.Ca PSM 227 |
| 9 | KYADKIYSI | Prost.Ca PSM 606 |
| 9 | NYARTEDFF | Prost.Ca PSM 178 |
| 9 | AYINADSSI | Prost.Ca PSM 448 |
| 9 | SASFCGSPY | HBV POL 165 |
| 9 | AFTFSPTYK | HBV POL 655 |
| 9 | SVVRRAFPH | HBV POL 524 |
| 9 | RWMCLRRFI | HBV ENV 236 |
| 9 | SWLSLLVPF | HBV ENV 334 |
| 9 | SWWTSLNFL | HBV ENV 197 |
| 9 | PWTHKVGNF | HBV POL 51 |
| 9 | SFCGSPYSW | HBV POL 167 |
| 10 | NADSSIEGNY | Prost.Ca PSM 451 |
| 10 | GLDSVELAHY | Prost.Ca PSM 104 |
| 10 | RATQIPSYKK | Prost.Ca PAP 273 |
| 10 | LGFLFGWFIK | Prost.Ca PSM 35 |
| 10 | SSIEGNYTLR | Prost.Ca PSM 454 |
| 10 | KSLYESWTKK | Prost.Ca PSM 491 |
| 10 | SLLSLYGIHK | Prost.Ca PAP 242 |
| 10 | FLYNFTQIPH | Prost.Ca PSM 73 |
| 10 | VIYAPSSHNK | Prost.Ca PSM 690 |
| 10 | AVVLRKYADK | Prost.Ca PSM 601 |
| 10 | KSPDEGFEGK | Prost.Ca PSM 482 |
| 10 | IVRSFGTLKK | Prost.Ca PSM 398 |
| 10 | RIYNVIGTLR | Prost.Ca PSM 354 |
| 10 | LSLYGIHKQK | Prost.Ca PAP 244 |
| 10 | MSLLKNRFLR | Prost.Ca PSA 99 |
| 10 | LSMKHPQEMK | Prost.Ca PSM 614 |
| 10 | RAVCGGVLVH | Prost.Ca PSA 43 |
| 10 | GSAPPDSSWR | Prost.Ca PSM 311 |
| 10 | SIPVHPIGYY | Prost.Ca PSM 291 |
| 10 | CSGKIVIARY | Prost.Ca PSM 196 |
| 10 | ETYELVEKFY | Prost.Ca PSM 557 |
| 10 | RLLQERGVAY | Prost.Ca PSM 440 |
| 10 | FYDPMFKYHL | Prost.Ca PSM 565 |
| 10 | TYSVSFDSLF | Prost.Ca PSM 624 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | LYNFTQIPHL | Prost.Ca PSM 74 |
| 10 | GWRPRRTILF | Prost.Ca PSM 409 |
| 10 | FAAPFTQCGY | HBV POL 631 |
| 10 | RWMCLRRFII | HBV ENV 236 |
| 10 | WFVGLSPTVW | HBV ENV 345 |
| 10 | SWPKFAVPNL | HBV POL 392 |
| 10 | VFADATPTGW | HBV POL 686 |
| 9 | FIFHKFQTK | HTLV-I tax 276 |
| 9 | FLTNVPYKR | HTLV-I tax 182 |
| 9 | ITWDPIDGR | HTLV-I tax 54 |
| 9 | SALQFLIPR | HTLV-I tax 66 |
| 9 | LSFPDPGLR | HTLV-I tax 131 |
| 9 | QSSSFIFHK | HTLV-I tax 272 |
| 9 | GLCSARLHR | HTLV-I tax 34 |
| 9 | RLPSFPTQR | HTLV-I tax 74 |
| 9 | AMRKYSPFR | HTLV-I tax 108 |
| 9 | ISGGLCSAR | HTLV-I tax 31 |
| 9 | ALFTAQEAK | HPV 16 E1 69 |
| 9 | ATMCRHYKR | HPV 16 E1 406 |
| 9 | FMSFLTALK | HPV 16 E1 453 |
| 9 | GVSFSELVR | HPV 16 E1 216 |
| 9 | KAAMLAKFK | HPV 16 E1 204 |
| 9 | LTNILNVLK | HPV 16 E1 191 |
| 9 | LVRPFKSNK | HPV 16 E1 222 |
| 9 | MSFLTALKR | HPV 16 E1 454 |
| 9 | NSNASAFLK | HPV 16 E1 386 |
| 9 | QMSMSQWIK | HPV 16 E1 419 |
| 9 | RLKAICIEK | HPV 16 E1 109 |
| 9 | SLFGMSLMK | HPV 16 E1 484 |
| 9 | SMSQWIKYR | HPV 16 E1 421 |
| 9 | TAAALYWYK | HPV 16 E1 315 |
| 9 | VVLLLVRYK | HPV 16 E1 274 |
| 9 | ALLRYKCGK | HPV 18 E1 284 |
| 9 | ATMCKHYRR | HPV 18 E1 413 |
| 9 | CATMCKHYR | HPV 18 E1 412 |
| 9 | FITFLGALK | HPV 18 E1 460 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | GVLILALLR | HPV 18 E1 279 |
| 9 | KLRAGQNHR | HPV 18 E1 647 |
| 9 | LILALLRYK | HPV 18 E1 281 |
| 9 | LTTNIHPAK | HPV 18 E1 571 |
| 9 | NMSQWIRFR | HPV 18 E1 428 |
| 9 | NSNAAAFLK | HPV 18 E1 393 |
| 9 | SVAALYWYR | HPV 18 E1 322 |
| 9 | WTYFDTYMR | HPV 18 E1 536 |
| 9 | YVQAIVDKK | HPV 18 E1 19 |
| 9 | IIKNFDIPK | GCDFP-15 36 |
| 9 | VLAVQTELK | GCDFP-15 55 |
| 10 | IIIKNFDIPK | GCDFP-15 35 |
| 10 | TACLCDDNPK | GCDFP-15 87 |
| 10 | AVLAVQTELK | GCDFP-15 54 |
| 10 | TFYWDFYTNR | GCDFP-15 97 |
| 9 | ASCHLTELY | PAP 311 |
| 10 | KGEYFVEMYY | PAP 322 |
| 10 | LTAAHCIRNK | PSA 57 |
| 9 | PLYDMSLLK | PSA 95 |
| 9 | QVHPQKVTK | PSA 182 |
| 9 | SLLKNRFLR | PSA 100 |
| 9 | YTKVVHYRK | PSA 239 |
| 9 | TLWKAGILY | HBV pol 150 |
| 9 | SLYTKVVHY | PSA 237 |
| 9 | PVNRPIDWK | HBV POL 612 |
| 9 | RHYLHTLWK | HBV POL 719 |
| 11 | HTLWKAGILYK | HBV POL 149 |
| 11 | GTDNSVVLSRK | HBV POL 735 |
| 11 | RVTGGVFLVDK | HBV POL 357 |
| 8 | ATQIPSYK | PAP 274 |
| 9 | WMNSTGFTK | HCV consensus |
| 9 | RVLEDGVNY | HCV consensus |
| 9 | RLLAPITAY | HCV consensus |
| 9 | GVLAALAAY | HCV consensus |
| 9 | RVCEKMALY | HCV consensus |

TABLE 8

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 1235.01 | 10 | AVFDRKSDAK |
| 26.0149 | 9 | CALRFTSAR |
| 26.0153 | 9 | SSAGPCALR |
| F104.02 | 9 | SLTPPHSAK |
| F105.01 | 9 | AIFQSSMTK |
| F105.02 | 9 | GIFQSSMTK |
| F105.03 | 9 | AAFQSSMTK |
| F105.04 | 9 | AIAQSSMTK |
| F105.05 | 9 | AIFASSMTK |
| F105.06 | 9 | AIFQASMTK |
| F105.07 | 9 | AIFQSAMTK |
| F105.08 | 9 | AIFQSSATK |
| F105.09 | 9 | AIFQSSMAK |
| F105.10 | 9 | AIFQSSMTA |
| F105.11 | 9 | FIFQSSMTK |
| F105.12 | 9 | SIFQSSMTK |
| F105.14 | 9 | ANFQSSMTK |
| F105.16 | 9 | AIFQCSMTK |
| F105.17 | 9 | AIFQSSMTR |
| F105.19 | 9 | AIFQSSMTY |
| F105.20 | 9 | AILQSSMTR |
| F105.21 | 9 | AIFQRSMTR |
| F105.24 | 10 | PAIFQSSMTK |
| F105.25 | 10 | AIFQSSMTKI |
| 27.0103 | 9 | AIILHQQQK |
| 27.0104 | 9 | YGFRLGFLH |
| 27.0108 | 9 | SSCMGGMNR |
| 27.0235 | 10 | TCTYSPALNK |
| 27.0239 | 10 | NSSCMGGMNR |
| 27.0240 | 10 | SSCMGGMNRR |
| 27.0250 | 10 | KSKKGQSTSR |
| 27.0252 | 10 | TSRHKKLMFK |
| 28.0062 | 8 | FMFSPTYK |
| 28.0063 | 8 | FVFSPTYK |
| 28.0066 | 8 | TMLXMXXK |

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 28.0322 | 9 | SMICSVVRR |
| 28.0323 | 9 | SVICSVVRR |
| 28.0324 | 9 | KVGNFTGLK |
| 28.0325 | 9 | KVGNFTGLR |
| 28.0326 | 9 | VVFFSQFSR |
| 28.0327 | 9 | SVNRPIDWK |
| 28.0328 | 9 | TLWKAGILK |
| 28.0329 | 9 | TLWKAGILR |
| 28.0330 | 9 | TMWKAGILY |
| 28.0331 | 9 | TVWKAGILY |
| 28.0332 | 9 | RMYLHTLWK |
| 28.0333 | 9 | RVYLHTLWK |
| 28.0334 | 9 | AMTFSPTYK |
| 28.0335 | 9 | AVTFSPTYK |
| 28.0336 | 9 | SVVRRAFPR |
| 28.0337 | 9 | SVVRRAFPK |
| 28.0338 | 9 | ISEYRHYXY |
| 28.0339 | 9 | GTGXNGWFY |
| 28.0340 | 9 | ASXHLTELY |
| 28.0341 | 9 | ASXDKXQLK |
| 28.0371 | 9 | RVXEKMALY |
| 28.0372 | 9 | XTGWFMVEA |
| 28.0374 | 9 | HISXLTFGR |
| 28.0375 | 9 | AVXTRGVAK |
| 28.0377 | 9 | HLIFXHSKK |
| 28.0378 | 9 | HTMLXMXXK |
| 28.0381 | 9 | RLKAIXIEK |
| 28.0383 | 9 | TLFXASDAK |
| 28.0384 | 9 | ALLRYKXGK |
| 28.0387 | 9 | ATMXRHYKR |
| 28.0388 | 9 | XATMXRHYK |
| 28.0390 | 9 | ATMXKHYRR |
| 28.0391 | 9 | LLAXAGLAY |
| 28.0392 | 9 | LAXAGLAYK |
| 28.0393 | 9 | SIVLPFDXR |
| 28.0394 | 9 | AAXWWAGIK |
| 28.0628 | 10 | QMFTFSPTYK |

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 28.0629 | 10 | QVFTFSPTYK |
| 28.0630 | 10 | TMWKAGILYK |
| 28.0631 | 10 | TVWKAGILYK |
| 28.0632 | 10 | VMGGVFLVDK |
| 28.0633 | 10 | VVGGVFLVDK |
| 28.0635 | 10 | SVLPETTVVR |
| 28.0638 | 10 | HTLWKAGILK |
| 28.0640 | 10 | HMLWKAGILY |
| 28.0395 | 9 | SAIXSVVRR |
| 28.0644 | 10 | GTFNSVVLSR |
| 28.0645 | 10 | YMFDVVLGAK |
| 28.0646 | 10 | MMWYWGPSLK |
| 28.0647 | 10 | MMWYWGPSLR |
| 28.0665 | 10 | IVGGWEXEK |
| 28.0667 | 10 | IILEXVYXK |
| 28.0668 | 10 | SIPHAAXHK |
| 28.0670 | 10 | IVXPIXSQK |
| 28.0671 | 10 | LIRXLRXQK |
| 28.0672 | 10 | XTYSPALNK |
| 28.0675 | 10 | TVXAGGXAR |
| 28.0676 | 10 | HISXLTFGR |
| 28.0677 | 10 | XVNXSQFLR |
| 28.0678 | 10 | LIFXHSKKK |
| 28.0679 | 10 | FVLGGXRHK |
| 28.0713 | 10 | TSAIXSVVRR |
| 28.0714 | 10 | HLIFXHSKKK |
| 28.0715 | 10 | LLIRXINXQK |
| 28.0716 | 10 | GIVXPIXSQK |
| 28.0717 | 10 | LLIRXLRXQK |
| 28.0718 | 10 | SLEQRSLHXK |
| 28.0720 | 10 | RIVGGWEXEK |
| 28.0721 | 10 | DIILEXVYXK |
| 28.0722 | 10 | XVYXKQQLLR |
| 28.0723 | 10 | RAVXGGVLVH |
| 28.0725 | 10 | LTAAHXIRNK |
| 28.0728 | 10 | KAAXWWAGIK |
| 28.0730 | 10 | VVRRXPHHER |

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 28.0731 | 10 | LLGIWGXSGK |
| 28.0732 | 10 | TTLFXASDAK |
| 28.0734 | 10 | RTVXAGGXAR |
| 28.0736 | 10 | GTQRXEKXSK |
| 28.0737 | 10 | LVQNANPDXK |
| 28.0738 | 10 | VTXGNGIQVR |
| 28.0739 | 10 | DXATMXRHYK |
| 28.0740 | 10 | GLAXHQLXAR |
| 28.0741 | 10 | ALLAXAGLAY |
| 28.0742 | 10 | LLAXAGLAYK |
| 28.0743 | 10 | XVARXPSGVK |
| 28.0745 | 10 | LVEIXTEMEK |
| 28.0746 | 10 | LLNWXMQIAK |
| 28.0824 | 11 | HMLWKAGILYK |
| 28.0825 | 11 | HVLWKAGILYK |
| 28.0826 | 11 | SMLPETTVVRR |
| 28.0827 | 11 | SVLPETTVVRR |
| 28.0828 | 11 | GMDNSVVLSRK |
| 28.0829 | 11 | GVDNSVVLSRK |
| 28.0830 | 11 | GTFNSVVLSRK |
| 28.0369 | 9 | GLAXHQLXA |
| 1259.02 | 9 | DTVDTVLEK |
| 1259.10 | 9 | PVTIGECPK |
| 1259.14 | 10 | FTAVGKEFNK |
| 1259.16 | 11 | RTLDFHDSNVK |
| 1259.21 | 11 | KTRPILSPLTK |
| 1259.26 | 11 | GTHPSSSAGLK |
| 1259.28 | 11 | ILWILDRLFFK |
| 1259.29 | 9 | WILDRLFFK |
| 1259.30 | 11 | CIYRRFKYGLK |
| 1259.31 | 9 | KSMREEYRK |
| 1259.33 | 9 | YIQMCTELK |
| 1259.37 | 10 | MVMELVRMIK |
| 1259.38 | 9 | VMELVRMIK |
| 1259.41 | 11 | LIRPNENPAHK |
| 26.0023 | 8 | VSFGVWIR |
| 26.0024 | 8 | VSIPWTHK |

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 26.0026 | 8 | ASFCGSPY |
| 26.0035 | 9 | TSPYELSLY |
| 26.0036 | 9 | TSIPFLHEY |
| 26.0041 | 9 | FNDPGPGTY |
| 26.0045 | 9 | YVDLGALRY |
| 26.0051 | 9 | DADRSFIEY |
| 26.0055 | 9 | NMDKAVKLY |
| 26.0056 | 9 | TTDNFYRNY |
| 26.0058 | 9 | HSAEALQKY |
| 26.0059 | 9 | LTAGLDFAY |
| 26.0061 | 9 | LTYKYNQFY |
| 26.0062 | 9 | CSNDKSLVY |
| 26.0063 | 9 | RSARASSRY |
| 26.0065 | 9 | ASADKPYSY |
| 26.0067 | 9 | STTAGPNEY |
| 26.0069 | 9 | LSGNGHFHY |
| 26.0073 | 9 | NTFVQANLY |
| 26.0074 | 9 | GTATYLPPY |
| 26.0081 | 9 | RLDAFRQTY |
| 26.0082 | 9 | KAEVHTFYY |
| 26.0083 | 9 | VAEGDTVIY |
| 26.0084 | 9 | LTEIDIRDY |
| 26.0085 | 9 | HTEFEGQVY |
| 26.0086 | 9 | VSDGGPNLY |
| 26.0092 | 9 | IIEDQYNRY |
| 26.0093 | 9 | FLDQWWTEY |
| 26.0095 | 9 | FVEDPNGKY |
| 26.0096 | 9 | ISDESYRVY |
| 26.0156 | 9 | YLAEADLSY |
| 26.0197 | 9 | ALLAVGATK |
| 26.0198 | 9 | ALNFPGSQK |
| 26.0199 | 9 | AVGATKVPR |
| 26.0203 | 9 | FSVSVSQLR |
| 26.0204 | 9 | GTATLRLVK |
| 26.0205 | 9 | GVSRQLRTK |
| 26.0207 | 9 | LIYRRRLMK |
| 26.0211 | 9 | QLVLHQILK |

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 26.0212 | 9 | SSHWLRLPR |
| 26.0214 | 9 | TMEVTVYHR |
| 26.0216 | 9 | VLASLIYRR |
| 26.0217 | 9 | VSCQGGLPK |
| 26.0218 | 9 | VVLASLIYR |
| 26.0227 | 9 | GTQCALTRR |
| 26.0251 | 9 | FTIPYWDWR |
| 26.0252 | 9 | GTPEGPLRR |
| 26.0253 | 9 | KSYLEQASR |
| 26.0255 | 9 | LVSLLCRHK |
| 26.0256 | 9 | MVPFIPLYR |
| 26.0258 | 9 | QTSAGHFPR |
| 26.0259 | 9 | SIFEQWLRR |
| 26.0260 | 9 | SLLCRHKRK |
| 26.0261 | 9 | SSWQIVCSR |
| 26.0267 | 10 | NMQIGGVLTY |
| 26.0273 | 10 | RMAQNFAMRY |
| 26.0274 | 10 | FTVQGSLSGY |
| 26.0275 | 10 | QTSPYELSLY |
| 26.0276 | 10 | SSNAILSLSY |
| 26.0280 | 10 | TSQPWWPADY |
| 26.0284 | 10 | VSDVSIIIPY |
| 26.0285 | 10 | ASDAQSANKY |
| 26.0286 | 10 | FTETNLAGEY |
| 26.0287 | 10 | YVDGFEPNGY |
| 26.0291 | 10 | FNDPGPGTYY |
| 26.0296 | 10 | FLDQWWTEYY |
| 26.0299 | 10 | AAEFATETAY |
| 26.0309 | 10 | NAEVVLNQLY |
| 26.0311 | 10 | FVDGDSLFEY |
| 26.0316 | 10 | PSEDAQVAVY |
| 26.0317 | 10 | MSDNIRTGLY |
| 26.0318 | 10 | ESELREILNY |
| 26.0319 | 10 | CMESVRNGTY |
| 26.0320 | 10 | KTENGITRLY |
| 26.0321 | 10 | LTEIDIRDYY |
| 26.0397 | 10 | LLVLMAVVLA |

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 26.0424 | 10 | AVVLASLIYR |
| 26.0425 | 10 | GALLAVGATK |
| 26.0426 | 10 | GTATLRLVKR |
| 26.0427 | 10 | HTMEVTVYHR |
| 26.0428 | 10 | IALNFPGSQK |
| 26.0432 | 10 | QLRALDGGNK |
| 26.0433 | 10 | QVPLDCVLYR |
| 26.0434 | 10 | SLIYRRRLMK |
| 26.0435 | 10 | SSSHWLRLPR |
| 26.0438 | 10 | TVSCQGGLPK |
| 26.0442 | 10 | VVLASLIYRR |
| 26.0466 | 10 | YVKVLHHTLK |
| 26.0473 | 10 | LIGCWYCRRR |
| 26.0474 | 10 | LLIGCWYCRR |
| 26.0485 | 10 | SSMHNALHIY |
| 26.0504 | 10 | CVSSKNLMEK |
| 26.0510 | 10 | FSSWQIVCSR |
| 26.0511 | 10 | GLVSLLCRHK |
| 26.0518 | 10 | YMVPFIPLYR |
| 26.0535 | 11 | GVWIRTPPAYR |
| 26.0539 | 11 | RLVVDFSQFSR |
| 26.0545 | 11 | TLPETTVVRRR |
| 26.0549 | 11 | LLPIFFCLWVY |
|  | 11 | STLPETTVVRR |
| 26.0550 | 11 | RAFPHCLAFSY |

Table 9

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| ALEAQQEAL | 9 | 1 | | 15 | 2.1 | | <0.0003 | | | |
| ILESLFRAV | 9 | 1 | | 93 | 2.1 | | 0.0004 | | | |
| VITKKVADL | 9 | 1 | | 101 | 2.1 | | <0.0003 | | | |
| CLGLSYDGL | 9 | 1/3 | | 174 | 2.1 | | 0.0004 | | | |
| QIMPKTGFL | 9 | 1 | | 187 | 2.1 | | 0.0007 | | | |
| SLHCKPEEAL | 10 | 1 | | 7 | 2.1 | | 0.0002 | | | |
| PLVLGTLEEV | 10 | 1 | | 37 | 2.1 | | 0.0008 | | | |
| CILESLFRAV | 10 | 1 | | 92 | 2.1 | | 0.0003 | | | |
| AVITKKVADL | 10 | 1 | | 100 | 2.1 | | 0 | | | |
| VITKKVADLV | 10 | 1 | | 101 | 2.1 | | 0 | | | |
| LLKYRAREPV | 10 | 1/3 | | 114 | 2.1 | | 0 | | | |
| EIFGKASESL | 10 | 1 | | 142 | 2.1 | | 0 | | | |
| CLGLSYDGLL | 10 | 1/3 | | 174 | 2.1 | | 0 | | | |
| AISRKMVEL | 9 | 2 | | 101 | 2.1 | | 0.0003 | | | |
| KMVELVHFL | 9 | 2 | | 105 | 2.1 | | 0.16 | | | |
| MVELVHFLL | 9 | 2 | | 106 | 2.1 | | 0.0031 | | | |
| DLQQSLRVL | 9 | 2 | | 143 | 2.1 | | 0 | | | |
| SLRVLAAGL | 9 | 2 | | 147 | 2.1 | | 0.0001 | | | |
| ALSRKVAEL | 9 | 3 | | 101 | 2.1 | | 0.0050 | | | |
| HLYIFATCL | 9 | 3 | | 167 | 2.1 | | 0.0003 | | | |
| YIFATCLGL | 9 | 3 | | 169 | 2.1 | | 0.018 | | | |
| QIMPKAGLL | 9 | 3 | | 187 | 2.1 | | 0 | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| AISRKMVELV | 10 | 2 | | 101 | 2.1 | | 0 | | | |
| MVELVHFLLL | 10 | 2 | | 106 | 2.1 | | 0.0017 | | | |
| KLPGLLSRDL | 10 | 2 | | 135 | 2.1 | | 0 | | | |
| LLSRDLQQSL | 10 | 2 | | 139 | 2.1 | | 0.0007 | | | |
| SLPTTMNYPL | 10 | 3 | | 63 | 2.1 | | 0.0035 | | | |
| DLESEFQAAL | 10 | 3 | | 93 | 2.1 | | 0.0001 | | | |
| ALSRKVAELV | 10 | 3 | | 101 | 2.1 | | 0.0001 | | | |
| KVAELVHFLL | 10 | 3 | | 105 | 2.1 | | 0.012 | | | |
| VIFSKASSSL | 10 | 3 | | 142 | 2.1 | | 0 | | | |
| SLQLVFGIEL | 10 | 3 | | 150 | 2.1 | | 0.0049 | | | |
| LMEVDPIGHL | 10 | 3 | | 159 | 2.1 | | 0.0005 | | | |
| FLIIVLVMI | 9 | 1 | | 194 | 2.1 | | 0.0005 | | | |
| GLLGDNQIM | 9 | 1 | | 181 | 2.1 | | 0.0051 | | | |
| SLHCKPEEA | 9 | 1 | | 7 | 2.1 | | 0.013 | <0.0002 | 0 | |
| ALGLVCVQA | 9 | 1 | | 22 | 2.1 | | 0.015 | <0.0002 | <0.0002 | |
| CKPEEALEA | 9 | 1 | | 10 | Random | | <0.0002 | | | |
| QQEALGLVC | 9 | 1 | | 19 | Random | | <0.0002 | | | |
| VQAATSSSS | 9 | 1 | | 28 | Random | | <0.0002 | | | |
| PLVLGTLEE | 9 | 1 | | 37 | Random | | <0.0002 | | | |
| VPTAGSTDP | 9 | 1 | | 46 | Random | | <0.0002 | | | |
| PQSPQGASA | 9 | 1 | | 55 | Random | | <0.0002 | | | |
| FPTTINFTR | 9 | 1 | | 64 | Random | | <0.0002 | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| QRQPSEGSS | 9 | 1 | | 73 | Random | | <0.0002 | | | |
| SREEEGPST | 9 | 1 | | 82 | Random | | <0.0002 | | | |
| AVITKKVAD | 9 | 1 | | 100 | Random | | <0.0002 | | | |
| EMLESVIKN | 9 | 1 | | 127 | Random | | <0.0002 | | | 0 |
| YKHCFPEIF | 9 | 1 | | 136 | Random | | <0.0002 | | | |
| GKASESLQL | 9 | 1 | | 145 | Random | | <0.0002 | | | |
| VFGIDVKEA | 9 | 1 | | 154 | Random | | <0.0002 | <0.0002 | 0 | |
| DPTGHSYVL | 9 | 1 | | 163 | Random | | <0.0002 | | | |
| VTCLGLSYD | 9 | 1 | | 172 | Random | | <0.0002 | | | |
| PKTGFLIIV | 9 | 1 | | 190 | Random | | <0.0002 | | | |
| LVMIAMEGG | 9 | 1 | | 199 | Random | | <0.0002 | | | |
| HAPEEEIWE | 9 | 1 | | 208 | Random | | <0.0002 | | | |
| ELSVMEVYD | 9 | 1 | | 217 | Random | | <0.0002 | | | |
| GREHSAYGE | 9 | 1 | | 226 | Random | | <0.0002 | | | |
| PRKLLTQDL | 9 | 1 | | 235 | Random | | 0.0002 | | | |
| VQEKYLEYG | 9 | 1 | | 244 | Random | | <0.0002 | | | |
| RCRTVIPHA | 9 | 1 | | 253 | Random | | <0.0002 | | | |
| MSSCGVQGP | 9 | 1 | | 262 | Random | | <0.0002 | | | |
| ILESLFRAVI | 10 | 1 | | 93 | 2.1 | | 0.0002 | | | |
| FLIIVLVMIA | 10 | 1 | | 194 | 2.1 | | 0.0003 | 0.0093 | 0.0030 | |
| LVFGIDVKEA | 10 | 1 | | 153 | 2.1 | | 0.0002 | <0.0002 | 0 | |
| EVYDGREHSA | 10 | 1 | | 222 | 2.1 | | 0 | <0.0002 | 0 | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| GVQGPSLKPA | 10 | 1 | | 266 | 2.1 | | 0.0001 | | | |
| QLVFGIDV | 8 | 1 | | 152 | 2.1 | | 0 | | | |
| KLLTQDLV | 8 | 1 | | 237 | 2.1 | | 0.0004 | | | |
| GLLGDNQI | 8 | 1 | | 181 | 2.1 | | 0 | | | |
| DLVGFLLL | 8 | 1 | | 108 | 2.1 | | 0 | | | |
| GLSYDGLL | 8 | 1 | | 176 | 2.1 | | 0.0001 | | | |
| DLVQEKYL | 8 | 1 | | 242 | 2.1 | | 0 | | | |
| LLGDNQIM | 8 | 1 | | 182 | 2.1 | | 0 | | | |
| FLIIVLVM | 8 | 1 | | 194 | 2.1 | | 0 | | | |
| ALEAQQEA | 8 | 1 | | 15 | 2.1 | | 0 | | | |
| TLEEVPTA | 8 | 1 | | 42 | 2.1 | | 0 | | | |
| IMPKTGFL | 8 | 1 | | 188 | 2.1 | | 0.0001 | | | |
| PVTKAEML | 8 | 1 | | 122 | 2.1 | | 0 | | | |
| IVLVMIAM | 8 | 1 | | 197 | 2.1 | | 0.0001 | | | |
| AVITKKVA | 8 | 1 | | 100 | 2.1 | | 0 | | | |
| EIWEELSV | 8 | 1 | | 213 | 2.1 | | 0 | | | |
| LIIVLVMI | 8 | 1 | | 195 | 2.1 | | 0.0001 | | | |
| IIVLVMIA | 8 | 1 | | 196 | 2.1 | | 0.0002 | | | |
| SLFRAVITKKV | 11 | 1 | | 96 | 2.1 | | 0.0001 | | | |
| LLLKYRAREPV | 11 | 1 | | 113 | 2.1 | | 0.0001 | | | |
| YLEYGRCRTVI | 11 | 1 | | 248 | 2.1 | | 0.0006 | | | |
| ALEAQQEALGL | 11 | 1 | | 15 | 2.1 | | 0.0001 | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| FLIIVLVMIAM | 11 | 1 | | 194 | 2.1 | | 0.0041 | | | |
| VLGTLEEVPTA | 11 | 1 | | 39 | 2.1 | | 0.0002 | | | |
| QLVFGIDVKEA | 11 | 1 | | 152 | 2.1 | | 0.0001 | | | |
| AVITKKVADLV | 11 | 1 | | 100 | 2.1 | | 0 | | | |
| PVTKAEMLESV | 11 | 1 | | 122 | 2.1 | | 0 | | | |
| KVADLVGFLLL | 11 | 1 | | 105 | 2.1 | | 0.020 | | | |
| GVQGPSLKPAM | 11 | 1 | | 266 | 2.1 | | 0 | | | |
| LVGFLLLKYRA | 11 | 1 | | 109 | 2.1 | | 0.0004 | | | |
| LVMIAMEGGHA | 11 | 1 | | 199 | 2.1 | | 0.0005 | | | |
| CILESLFRAVI | 11 | 1 | | 92 | 2.1 | | 0.0030 | | | |
| EALEAQQEA | 9 | 1 | | 14 | 2.1 | | 0 | <0.0002 | 0 | |
| EAQQEALGL | 9 | 1 | | 17 | 2.1 | | 0 | | | <0.0002 |
| AATSSSSPL | 9 | 1 | | 30 | 2.1 | | 0 | | | <0.0002 |
| ATSSSSPLV | 9 | 1 | | 31 | 2.1 | | 0.0007 | | | |
| GTLEEVPTA | 9 | 1 | | 41 | 2.1 | | 0.013 | <0.0002 | 0 | |
| GASAFPTTI | 9 | 1 | | 60 | 2.1 | | 0 | | | <0.0002 |
| STSCILESL | 9 | 1 | | 89 | 2.1 | | 0.0002 | | | |
| RAVITKKVA | 9 | 1 | | 99 | 2.1 | | 0 | <0.0002 | 0 | |
| ITKKVADLV | 9 | 1 | | 102 | 2.1 | | 0 | | | |
| RAREPVTKA | 9 | 1 | | 118 | 2.1 | | 0 | | | |
| KAEMLESVI | 9 | 1 | | 125 | 2.1 | | 0 | | | <0.0002 |
| KASESLQLV | 9 | 1 | | 146 | 2.1 | | 0.0009 | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| PTGHSYVLV | 9 | 1 | | 164 | 2.1 | | 0 | | | |
| KTGFLIIVL | 9 | 1 | | 191 | 2.1 | | 0.0006 | | | |
| LIIVLVMIA | 9 | 1 | | 195 | 2.1 | | 0 | 0.0022 | 0.0006 | |
| IIVLVMIAM | 9 | 1 | | 196 | 2.1 | | 0.0007 | | | |
| MIAMEGGHA | 9 | 1 | | 201 | 2.1 | | 0.0005 | <0.0002 | 0.0002 | |
| EIWEELSVM | 9 | 1 | | 213 | 2.1 | | 0 | | | <0.0002 |
| SAYGEPRKL | 9 | 1 | | 230 | 2.1 | | 0.0002 | | | |
| YLEYGRCRT | 9 | 1 | | 248 | 2.1 | | 0 | | | |
| EALGLVCVQA | 10 | 1 | | 21 | 2.1 | | 0.0005 | <0.0002 | 0 | |
| QAATSSSSPL | 10 | 1 | | 29 | 2.1 | | 0 | | | <0.0002 |
| VTKAEMLESV | 10 | 1 | | 123 | 2.1 | | 0 | | | |
| EADPTGHSTV | 10 | 1 | | 161 | 2.1 | | 0 | | | |
| VLGTLEEVPT | 10 | 1 | | 39 | 2.1 | | 0.0004 | | | |
| SAFPTTINFT | 10 | 1 | | 62 | 2.1 | | 0 | | | |
| GIDVKEADPT | 10 | 1 | | 156 | 2.1 | | 0 | | | |
| PTGHSYVLVT | 10 | 1 | | 164 | 2.1 | | 0 | | | |
| FLWGPRALA | 9 | 1 | new | 265 | 2.1 | | 0.042 | 0.0017 | 0 | |
| LAETSYVKV | 9 | 1 | new | 272 | 2.1 | | 0 | | | |
| YVKVLEYVI | 9 | 1 | new | 277 | 2.1 | | 0.0002 | | | |
| RVRFFFPSL | 9 | 1 | new | 290 | 2.1 | | 0.0001 | | | |
| LAETSYVKVL | 10 | 1 | new | 272 | 2.1 | | 0 | | | <0.0002 |
| VLEYVIKVSA | 10 | 1 | new | 280 | 2.1 | | 0.0002 | 0.0002 | 0 | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| AALREEEEGV | 10 | 1 | new | 301 | 2.1 | | 0 | | | |
| SMHCKPEEV | 9 | 1 | new (a) | 7 | 2.1 | | 0.018 | | | |
| AMGLVCVQV | 9 | 1 | new (a) | 22 | 2.1 | | 0.012 | | | |
| LMLGTLEEV | 9 | 1 | new (a) | 38 | 2.1 | | 0.13 | | | |
| LQLVFGIDV | 9 | 1 | new | 151 | 2.1 | | 0.0004 | | | |
| GLSYDGLLG | 9 | 1 | new | 176 | 2.1 | | 0 | | | |
| GLSYDGLLV | 9 | 1 | new (a) | 176 | 2.1 | | 0.0047 | | | |
| LLGDNQIMP | 9 | 1 | new | 182 | 2.1 | | 0.0001 | | | |
| LLGDNQIMV | 9 | 1 | new (a) | 182 | 2.1 | | 0.043 | | | |
| WEELSVMEV | 9 | 1 | new | 215 | 2.1 | | 0 | | | |
| WMELSVMEV | 9 | 1 | new (a) | 215 | 2.1 | | 0.041 | | | |
| RKLLTQDLV | 9 | 1 | new | 236 | 2.1 | | 0 | | | |
| YEFLWGPRA | 9 | 1 | new | 262 | 2.1 | | 0 | | | |
| YMFLWGPRV | 9 | 1 | new (a) | 262 | 2.1 | | 0.22 | | | |
| AATSSSSPLV | 10 | 1 | new | 30 | 2.1 | | 0 | | | |
| ATSSSSPLVL | 10 | 1 | new | 31 | 2.1 | | 0 | | | |
| KMADLVGFLV | 10 | 1 | new (a) | 105 | 2.1 | | 1.5 | | | |
| VADLVGFLLL | 10 | 1 | new | 106 | 2.1 | | 0.0008 | | | 0.0003 |
| SESLQLVFGI | 10 | 1 | new | 148 | 2.1 | | 0 | | | |
| VMVTCLGLSV | 10 | 1 | new (a) | 170 | 2.1 | | 0.30 | | | |
| QIMPKTGFLI | 10 | 1 | new | 187 | 2.1 | | 0.0009 | | | |
| QMMPKTGFLV | 10 | 1 | new (a) | 187 | 2.1 | | 0.050 | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| KTGFLIIVLV | 10 | 1 | new | 191 | 2.1 | | 0.0012 | | | |
| LIIVLVMIAM | 10 | 1 | new | 195 | 2.1 | | 0.0003 | | | |
| VMIAMEGGHV | 10 | 1 | new (a) | 200 | 2.1 | | 0.053 | | | |
| SAYGEPRKLL | 10 | 1 | new | 230 | 2.1 | | 0 | | | 0.0008 |
| ALAETSYVKVL | 11 | 1 N | | 270 | 2.1 | | 0.012 | | | |
| KMVELVHFLLL | 11 | 2 | | 52 | 2.1 | | 0.67 | | | |
| ELMEVDPIGHL | 11 | 3 | | 105 | 2.1 | | 0.026 | | | |
| HLYIFATCLGL | 11 | 3 | | 114 | 2.1 | | 0.041 | | | |
| LLLKYRAREPV | 11 | 3 | | 60 | 2.1 | | 0.0001 | | | |
| QLVFGIELMEV | 11 | 3 | | 99 | 2.1 | | 0.34 | | | |
| IMPKAGLLIIV | 11 | 3 | | 135 | 2.1 | | 0.013 | | | |
| VLVTCLGLSYDGL | 13 | 1 n | E6 | 170 | 2.1 | | 0.0017 | | | |
| KLLTQDLVQEKYL | 13 | 1 n | E6 | 237 | 2.1 | | 0.0060 | | | |
| DLVQEKYLEYRQV | 13 | 1 n | E6 | 242 | 2.1 | | 0 | | | |
| SLFRAVITKKVADLV | 15 | 1 n | POL | 96 | 2.1 | | 0.0004 | | | |
| DLESEFQAAISRKMV | 15 | 2 | POL | 40 | 2.1 | | 0 | | | |
| MLGSVVGNWQYFFPV | 15 | 3 | POL | 75 | 2.1 | | 0.012 | | | |
| GASSFSTTI | 9 | 2 | | 60 | 2.1 | | 0 | | | 0.0002 |
| DLESEFQAA | 9 | 2,3 | | 93 | 2.1 | | 0 | | | |
| QAAISRKMV | 9 | 2 | | 99 | 2.1 | | 0 | | | |
| KAEMLESVL | 9 | 2 | | 125 | 2.1 | | 0 | | | 0 |
| KASEYLQLV | 9 | 2 | | 146 | 2.1 | | 0.011 | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| QLVFGIEVV | 9 | 2 | | 152 | 2.1 | | 0.0038 | | | |
| VVPISHLYI | 9 | 2 | | 162 | 2.1 | | 0.0002 | | | |
| PISHLYILV | 9 | 2 | | 164 | 2.1 | | 0.0005 | | | |
| HLYILVTCL | 9 | 2 | | 167 | 2.1 | | 0.0034 | | | |
| YILVTCLGL | 9 | 2 | | 169 | 2.1 | | 0.0014 | | | |
| GLLGDNQVM | 9 | 2 | | 181 | 2.1 | | 0.0038 | | | |
| QVMPKTGLL | 9 | 2 | | 187 | 2.1 | | 0 | | | |
| VMPKTGLLI | 9 | 2 | | 188 | 2.1 | | 0.0010 | | | 0.230 |
| KTGLLIIVL | 9 | 2 | | 191 | 2.1 | | 0.0002 | | | |
| GLLIIVLAI | 9 | 2,3 | | 193 | 2.1 | | 0.0002 | | | |
| LLIIVLAII | 9 | 2,3 | | 194 | 2.1 | | 0.0001 | | | |
| LIIVLAIIA | 9 | 2,3 | | 195 | 2.1 | | 0.0008 | | | |
| IIVLAIIAI | 9 | 2 | | 196 | 2.1 | | 0.0009 | | | |
| IIAIEGDCA | 9 | 2 | | 201 | 2.1 | | 0 | | | |
| GASSLPTTM | 9 | 3 | | 60 | 2.1 | | 0 | | | 0.0010 |
| QAALSRKVA | 9 | 3 | | 99 | 2.1 | | 0 | | | |
| VAELVHFLL | 9 | 3 | | 106 | 2.1 | | 0 | | | 0.039 |
| KAEMLGSVV | 9 | 3 | | 125 | 2.1 | | 0 | | | |
| KASSSLQLV | 9 | 3 | | 146 | 2.1 | | 0.0005 | | | |
| QLVFGIELM | 9 | 3 | | 152 | 2.1 | | 0.0010 | | | |
| PIGHLYIFA | 9 | 3 | | 164 | 2.1 | | 0 | | | |
| IMPKAGLLI | 9 | 3 | | 188 | 2.1 | | 0.0064 | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| KAGLLIIVL | 9 | 3 | | 191 | 2.1 | | 0.0002 | | | 0 |
| IIAREGDCA | 9 | 3 | | 201 | 2.1 | | 0 | | | |
| EALEAQQEAL | 10 | 1 | new | 14 | 2.1 | | 0 | | | 0 |
| EAQQEALGLV | 10 | 1 | new | 17 | 2.1 | | 0 | | | |
| DLESEFQAAI | 10 | 2 | | 93 | 2.1 | | 0 | | | |
| AAISRKMVEL | 10 | 2 | | 100 | 2.1 | | 0 | | | 0 |
| VIFSKASEYL | 10 | 2 | | 142 | 2.1 | | 0.0014 | | | |
| YLQLVFGIEV | 10 | 2 | | 150 | 2.1 | | 0.37 | | | |
| LVFGIEVVEV | 10 | 2 | | 153 | 2.1 | | 0.012 | | | |
| GIEVVEVVPI | 10 | 2 | | 156 | 2.1 | | <0.0002 | | | |
| VVEVVPISHL | 10 | 2 | | 159 | 2.1 | | <0.0002 | | | |
| EVVPISHLYI | 10 | 2 | | 161 | 2.1 | | <0.0002 | | | |
| VVPISHLYIL | 10 | 2 | | 162 | 2.1 | | 0.0002 | | | |
| PISHLYILVT | 10 | 2 | | 164 | 2.1 | | 0.0003 | | | |
| QVMPKTGLLI | 10 | 2 | | 187 | 2.1 | | 0.0002 | | | |
| VMPKTGLLII | 10 | 2 | | 188 | 2.1 | | 0.0009 | | | 0.058 |
| KTGLLIIVLA | 10 | 2 | | 191 | 2.1 | | <0.0002 | | | |
| GLLIIVLAII | 10 | 2,3 | | 193 | 2.1 | | 0.0005 | | | |
| LLIIVLAIIA | 10 | 2,3 | | 194 | 2.1 | | <0.0002 | | | |
| LIIVLAIIAI | 10 | 2 | | 195 | 2.1 | | 0.0013 | | | |
| AIIAIEGDCA | 10 | 2 | | 200 | 2.1 | | 0.0023 | | | |
| AALSRKVAEL | 10 | 3 | | 100 | 2.1 | | 0.0007 | | | 0 |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| VAELVHFLLL | 10 | 3 | | 106 | 2.1 | | 0.0009 | | | 0.0018 |
| VTKAEMLGSV | 10 | 3 | | 123 | 2.1 | | <0.0002 | | | |
| GIELMEVDPI | 10 | 3 | | 156 | 2.1 | | <0.0002 | | | |
| EVDPIGHLYI | 10 | 3 | | 161 | 2.1 | | <0.0002 | | | |
| PIGHLYIFAT | 10 | 3 | | 164 | 2.1 | | 0.0003 | | | |
| QIMPKAGLLI | 10 | 3 | | 187 | 2.1 | | 0.0006 | | | |
| IMPKAGLLII | 10 | 3 | | 188 | 2.1 | | 0.0015 | | | |
| KAGLLIIVLA | 10 | 3 | | 191 | 2.1 | | <0.0002 | | | |
| AIIAREGDCA | 10 | 3 | | 200 | 2.1 | | <0.0002 | | | |
| FLWGPRALI | 9 | 2 | | 271 | A02 | | | | | |
| GLEARGEAL | 9 | 3 | | 15 | A02 | | | | | |
| EARGEALGL | 9 | 3 | | 17 | A02 | | | | | |
| ALGLVGAQA | 9 | 3 | | 22 | A02/A03 | | | | | |
| GLVGAQAPA | 9 | 3 | | 24 | A02/A03 | | | | | |
| LVGAQAPAT | 9 | 3 | | 25 | A02 | | | | | |
| PATEEQEAA | 9 | 3 | | 31 | A02/A03 | | | | | |
| EAASSSSTL | 9 | 3 | | 37 | A02 | | | | | |
| AASSSSTLV | 9 | 3 | | 38 | A02 | | | | | |
| LVEVTLGEV | 9 | 3 | | 45 | A02 | | | | | |
| EVTLGEVPA | 9 | 3 | | 47 | A02/A03 | | | | | |
| VTLGEVPAA | 9 | 3 | | 48 | A02/A03 | | | | | |
| KIWEELSVL | 9 | 3 | | 220 | A02 | | | | | |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| SILGDPKKL | 9 | 3 | | 237 | A02 | | | | | |
| ILGDPKKLL | 9 | 3 | | 238 | A02 | | | | | |
| FLWGPRALV | 9 | 3 | | 271 | A02 | | | | | |
| RALVETSYV | 9 | 3 | | 276 | A02 | | | | | |
| LVETSYVKV | 9 | 3 | | 278 | A02 | | | | | |
| YVKVLHHMV | 9 | 3 | | 283 | A02 | | | | | |
| KVLHHMVKI | 9 | 3 | | 285 | A02 | | | | | |
| EARGEALGLV | 10 | 3 | | 17 | A02 | | | | | |
| EALGLVGAQA | 10 | 3 | | 21 | A02/A03 | | | | | |
| GLVGAQAPAT | 10 | 3 | | 24 | A02 | | | | | |
| QAPATEEQEA | 10 | 3 | | 29 | A02/A03 | | | | | |
| EAASSSSTLV | 10 | 3 | | 37 | A02 | | | | | |
| TLVEVTLGEV | 10 | 3 | | 44 | A02 | | | | | |
| EVTLGEVPAA | 10 | 3 | | 47 | A02/A03 | | | | | |
| EVPEGREDSI | 10 | 3 | | 229 | A02 | | | | | |
| SILGDPKKLL | 10 | 3 | | 237 | A02 | | | | | |
| ILGDPKKLLT | 10 | 3 | | 238 | A02 | | | | | |
| ALVETSYVKV | 10 | 3 | | 277 | A02 | | | | | |
| LVETSYVKVL | 10 | 3 | | 278 | A02 | | | | | |
| MVKISGGPHI | 10 | 3 | | 290 | A02 | | | | | |
| LVLGTLEEV | 9 | 1 | | 38 | 2.1 | <0.0006 | 0.032 | 0 | 0 | 0.0003 |
| KVADLVGFLL | 10 | 1 | | 105 | | 0.0005 | 0.041 | 0.0039 | 0.0030 | 0.0070 |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| LVFGIELMEV | 10 | 3 | | 153 | 2.1 | | 0.17 | | | |
| ILLWQPIPV | 9 | 3 | | | | <0.0007 | 1.4 | 0.0048 | 0.0048 | 0 |
| EVDPIGHLY | 9 | 3 | | | | 3.7 | | | 0.0022 | |
| KMVELVHFL | 9 | 2 | | | | <0.0007 | 0.13 | 0.0007 | 0 | 0.0043 |
| KMVELVHFLL | 10 | 2 | | 105 | | <0.0008 | 0.071 | 0.0004 | 0.0001 | 0.0008 |
| LVFGIELMEV | 10 | 3 | | | | 0.0030 | 0.065 | 0.0007 | 0 | 0 |
| KVAELVHFL | 9 | 3 | | 105 | 2.1 | 0 | 0.073 | 0.011 | 0.0047 | 0.0005 |
| CILESLFRA | 9 | 1 | | 92 | 2.1 | 0.0001 | 0.073 | 0 | 0.0002 | 0 |
| VMIAMEGGHA | 10 | 1 | | 200 | 2.1 | <0.00008 | 0.0023 | 0 | 0 | 0 |
| MLESVIKNYK | 10 | 1 | | | | 0 | 0 | 0.034 | 0.0045 | 0 |
| ETSYVKVLEY | 10 | 1 | | | | 0.075 | 0 | 0.0009 | 0.0004 | 0 |
| KVLEYVIKV | 9 | 1 | new | 279 | 2.1 | <0.0005 | 0.095 | 0.022 | 0.015 | 0 |
| FLWGPRALA | 9 | 1 | | | | <0.0006 | 0.027 | 0.0015 | 0 | 0 |
| ALREEEEGV | 9 | 1 | | 302 | 2.1 | <0.0006 | 0.0056 | 0 | 0 | 0 |
| ALAETSYVKV | 10 | 1 | | 271 | | <0.0007 | 0.017 | 0.0011 | 0.0029 | 0 |
| YVIKVSARV | 9 | 1 | | 283 | 2.1 | 0.0005 | 0.018 | 0 | 0 | 0 |
| RALAETSYV | 9 | 1 | | 270 | 2.1 | <0.0006 | 0.014 | 0.0003 | 0.0005 | 0 |
| ALAETSYVK | 9 | 1 | | | | <0.0006 | 0.0002 | 0.17 | 0.39 | 0 |
| VLGTLEEV | 8 | 1 | | 39 | 2.1 | <0.0007 | 0.0088 | 0 | 0 | 0 |
| SLQLVFGI | 8 | 1 | | 150 | 2.1 | <0.0007 | 0.0094 | 0 | 0.0001 | 0 |
| ILESLFRA | 8 | 1 | | 93 | 2.1 | <0.0004 | 0.0017 | 0.0003 | 0 | 0.0001 |
| FLLLKYRA | 8 | 1 | | 112 | 2.1 | 0.0036 | 0.0007 | 0.0003 | 0.0001 | 0 |

| Sequence | AA | Mage Strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| GLVCVQAA | 8 | 1 | | 24 | 2.1 | 0.0016 | 0.0008 | 0.0008 | 0 | 0 |
| VLVTCLGL | 8 | 1 | | 170 | 2.1 | <0.0007 | 0.0010 | 0.0001 | 0 | 0 |
| KVADLVGFL | 9 | 1 | | 105 | 2.1 | <0.0008 | 0.0091 | 0.0013 | 0.0005 | 0 |
| YVLVTCLGL | 9 | 1 | | 169 | 2.1 | | | | | |
| IMPKTGFLI | 9 | 1 | | 188 | 2.1 | <0.0008 | 0.0035 | 0 | 0 | 3.2 |
| GLLGDNQIM | 9 | 1 | | | A2.1 | <0.0008 | 0.0054 | 0 | 0 | 0.0002 |
| GLVCVQAAT | 9 | 1 | | 24 | 2.1 | 0.0030 | 0.0007 | 0.0026 | 0 | 0.0001 |
| VADLVGFLL | 9 | 1 | | 106 | 2.1 | 0.032 | 0.0011 | 0.0054 | 0.0008 | 0.0007 |
| YLEYGRCRTV | 10 | 1 | | 248 | 2.1 | 0.0008 | 0.0097 | 0.0001 | 0 | 0 |
| SLQLVFGIDV | 10 | 1 | | 150 | 2.1 | 0.0028 | 0.0047 | 0.0013 | 0.0001 | 0.0001 |
| IMPKTGFLII | 10 | 1 | | 188 | 2.1 | <0.0008 | 0.0007 | 0 | 0 | 0.050 |
| ALGLVCVQAA | 10 | 1 | | 22 | A2.1 | 0.0011 | 0.0002 | 0.0003 | 0 | 0 |
| EIWEELSVMEV | 11 | 1 | | 213 | A2.1 | 0.0007 | 0.013 | 0.0001 | 0.0001 | 0 |
| FLIIVLVMIAM | 11 | 1 | | | A2.1 | 0.023 | 0.0031 | 0.016 | 0.0014 | 0.0011 |
| VIPHAMSSCGV | 11 | 1 | | 257 | 2.1 | <0.0009 | 1.4 | 0 | 0 | 0 |
| CILESCFRAVI | 11 | 1 | | | A2.1 | 0.079 | 0.0017 | 0.058 | 0.0005 | 0.0008 |
| QIMPKTGFLII | 11 | 1 | | 187 | 2.1 | <0.0009 | 0.0003 | 0 | 0 | 0.0030 |
| GFLLLKYRA | 9 | 1 | | | | | | 0.0004 | 0.0002 | |
| CFPEIFGKA | 9 | 1 | | | | | | 0 | 0 | |
| FFFPSLREA | 9 | 1 | | | | | | 0 | 0 | |
| FFPSLREAA | 9 | 1 | | | | | | 0 | 0 | |
| RSLHCKPEEA | 10 | 1 | | | | | | 0.0001 | 0.0008 | |

| Sequence | AA | Mage strain | Mol. | Pos. | Motif | A1 | A2.1 | A3.2 | A11 | A24 |
|---|---|---|---|---|---|---|---|---|---|---|
| EFLWGPRALA | 10 | 1 | | | | | | 0 | 0 | |
| RFFFPSLREA | 10 | 1 | | | | | | 0.0004 | 0 | |
| FFFPSLREAA | 10 | 1 | | | | | | 0 | 0 | |

| Sequence | Antigen | Strain | Molecule | Position | Motif | A1 Binding | A2 Binding | A3 Binding | A11 Binding | A24 Binding | Max. Binding |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ALFLGFLGAA | HIV | MN | gp160 | 518 | A02 | | 0.49501 | | | | 0.49501 |
| MLQLTVWGI | HIV | MN | gp160 | 566 | A02 | | 0.24501 | | | | 0.24501 |
| RVIEVLQRA | HIV | MN | gp160 | 829 | A02 | | 0.19603 | | | | 0.19603 |
| KLTPLCVTL | HIV | MN | gp160 | 120 | A02 | | 0.16001 | | | | 0.16001 |
| LLIAARIVEL | HIV | MN | gp160 | 776 | A02 | | 0.15501 | | | | 0.15501 |
| SLLNATDIAV | HIV | MN | gp160 | 814 | A02 | | 0.10501 | | | | 0.10501 |
| ALFLGFLGA | HIV | MN | gp160 | 518 | A02 | | 0.09405 | | | | 0.09405 |
| HMLQLTVWGI | HIV | MN | gp160 | 565 | A02 | | 0.06677 | | | | 0.06677 |
| LLNATDIAV | HIV | MN | gp160 | 815 | A02 | | 0.06007 | | | | 0.06007 |
| ALLYKLDIV | HIV | MN | gp160 | 179 | A02 | | 0.03620 | | | | 0.03620 |
| WLWYIKIFI | HIV | MN | gp160 | 679 | A02 | | 0.03555 | | | | 0.03555 |
| TIIVHLNESV | HIV | MN | gp160 | 288 | A02 | | 0.03501 | | | | 0.03501 |
| LLQYWSQEL | HIV | MN | gp160 | 800 | A02 | | 0.02650 | | | | 0.02650 |
| IMIVGGLVGL | HIV | MN | gp160 | 687 | A02 | | 0.02520 | | | | 0.02520 |
| LLYKLDIVSI | HIV | MN | gp160 | 180 | A02 | | 0.02450 | | | | 0.02450 |
| FLAIIWVDL | HIV | MN | gp160 | 753 | A02 | | 0.02330 | | | | 0.02330 |
| TLQCKIKQII | HIV | MN | gp160 | 415 | A02 | | 0.02001 | | | | 0.02001 |
| GLVGLRIVFA | HIV | MN | gp160 | 692 | A02 | | 0.01950 | | | | 0.01950 |
| FLGAAGSTM | HIV | MN | gp160 | 523 | A02 | | 0.01900 | | | | 0.01900 |
| IISLWDQSL | HIV | MN | gp160 | 107 | A02 | | 0.01790 | | | | 0.01790 |
| TVWGIKQLQA | HIV | MN | gp160 | 570 | A02 | | 0.01501 | | | | 0.01501 |
| LLGRRGWEV | HIV | MN | gp160 | 785 | A02 | | 0.01420 | | | | 0.01420 |
| AVLSIVNRV | HIV | MN | gp160 | 701 | A02 | | 0.01320 | | | | 0.01320 |

| Sequence | Antigen | Strain | Molecule | Position | Motif | A1 | A2 | A3 | A11 | A24 | Max. |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Binding | Binding | Binding | Binding | Binding | Binding |
| FIMIVGGLV | HIV | MN | gp160 | 686 | A02 | | 0.0131 | | | | 0.0131 |
| LLNATDIAVA | HIV | MN | gp160 | 815 | A02 | | 0.0117 | | | | 0.0117 |
| FLYGALLLA | PLP | Human | | 80 | A02 | | 1.9000 | | | | 1.9000 |
| SLLTFMIAA | PLP | Human | | 253 | A02 | | 0.5300 | | | | 0.5300 |
| FMIAATYNFAV | PLP | Human | | 257 | A02 | | 0.4950 | | | | 0.4950 |
| RMYGVLPWI | PLP | Human | | 205 | A02 | | 0.1650 | | | | 0.1650 |
| IAATYNFAV | PLP | Human | | 259 | A02 | | 0.0540 | | | | 0.0540 |
| GLLECCARCLV | PLP | Human | | 2 | A02 | | 0.0515 | | | | 0.0515 |
| YALTVVWLL | PLP | Human | | 157 | A02 | | 0.0415 | | | | 0.0415 |
| ALTVVWLLV | PLP | Human | | 158 | A02 | | 0.0390 | | | | 0.0390 |
| FLYGALLL | PLP | Human | | 80 | A02 | | 0.0345 | | | | 0.0345 |
| SLCADARMYGV | PLP | Human | | 199 | A02 | | 0.0140 | | | | 0.0140 |
| LLVFACSAV | PLP | Human | | 164 | A02 | | 0.0107 | | | | 0.0107 |

Table 10

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | YIFATCLGL | MAGE 3 169 |
| 9 | IMPKTGFLI | MAGE 1 188 |
| 10 | IMPKTGFLII | MAGE 1 188 |
| 15 | MLGSVVGNWQYFFPV | MAGE 3 POL 75 |
| 9 | VMPKTGLLI | MAGE 2 188 |
| 9 | IMPKAGLLI | MAGE 3 188 |
| 10 | IMPKAGLLII | MAGE 3 188 |
| 9 | RLWHYPCTV | HCV Env2 614 |
| 9 | RLWHYPCTI | HCV Env2 614 |
| 9 | FLLLADARI | HCV Env2 |
| 9 | GVWPLLLLL | HCV Env2 792 |
| 9 | GMWPLLLLL | HCV Env2 792 |
| 9 | YLNTPGLPV | HCV NS3/NS4 1542 |
| 9 | YMNTPGLPV | HCV NS3/NS4 1542 |
| 9 | VILDSFDPL | HCV NS5 2251 |
| 9 | ILMTHFFSI | HCV NS5 2843 |
| 9 | ILMTHFFSV | HCV NS5 2843 |
| 9 | LMAVVLASL | gp100 606 |
| 9 | SLSLGFLFL | PAP 13 |
| 10 | YMIMVKCWMI | c-ErbB2 952 |
| 10 | GLHGQDLFGI | PAP 196 |
| 9 | AILSVSSFL | P. falciparum CSP 6 |
| 9 | GLIMVLSFL | P. falciparum CSP 425 |
| 9 | VLLGGVGLV | P. falciparum EXP-1 91 |
| 9 | GLLGNVSTV | P. falciparum EXP-1 83 |
| 9 | LLGNVSTVL | P. falciparum EXP-1 84 |
| 9 | VLAGLLGNV | P. falciparum EXP-1 80 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | KILSVFFLA | P. falciparum EXP-1 2 |
| 9 | FLIFFDLFL | P. falciparum TRAP 14 |
| 9 | LIFFDLFLV | P. falciparum TRAP 15 |
| 9 | FMKAVCVEV | P. falciparum TRAP 230 |
| 9 | LLMDCSGSI | P. falciparum TRAP 51 |
| 10 | ILSVSSFLFV | P. falciparum CSP 7 |
| 10 | VLLGGVGLVL | P. falciparum EXP-1 91 |
| 10 | GLLGNVSTVL | P. falciparum EXP-1 83 |
| 10 | FLIFFDLFLV | P. falciparum TRAP 14 |
| 10 | GLALLACAGL | P. falciparum TRAP 507 |
| 9 | KIWEELSML | MAGE2 220 |
| 9 | TLMSAMTNL | Prost.Ca PAP 112 |
| 9 | LLLARAASL | Prost.Ca PAP 6 |
| 9 | ALDVYNGLL | Prost.Ca PAP 299 |
| 9 | VTWIGAAPL | PSA 8 |
| 10 | ALIETSYVKV | MAGE2 277 |
| 10 | SLSLGFLFLL | Prost.Ca PAP 13 |
| 10 | RTLMSAMTNL | PAP 111 |
| 10 | FLPSDFFPSV(CONH2) | HBc 18-27 |
| 10 | FLPSDFFPSV-NH2 | HBc 18-27 |
| 9 | ILGFVFTLT-NH2 | Flu Matrix 59-67 |
| 10 | KGILGFVFTL-NH2 | Flu Matrix 57-66 |
| 11 | FLPSDFFPSVR | HBc 18-28 |
| 9 | FLPSDFFPS | HBc 18-26 |
| 9 | GILGKVFTL | Flu Matrix 58-66 analog |
| 9 | FLSKQYLNL | HBV polymerase |
| 9 | KLQCVPLHV | PSA 166-174 P/D |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | KLQCVPLHV | PSA 166-174 P/D |
| 9 | KLQCVPLHV | PSA 166-174 P/D |
| 9 | KLYEIVAKV | A2.1 consensus |
| 9 | KLAEYVAKV | A2.1 consensus |
| 9 | KLAEIVYKV | A2.1 consensus |
| 9 | TLTSCNTSV | HIV gp 120 env. RE trans. 197 |
| 9 | ALMEKIYQV | A2.1 consensus peptide |
| 9 | ALSEKIYQV | A2.1 consensus peptide |
| 9 | FLMSYFPSV | 941.01 9-mer analog |
| 9 | FLPSYFPSV | 941.01 9-mer analog |
| 10 | FLMSDYFPSV | 941.01 M2 analog |
| 9 | FLYCYFALV | Chiron consensus |
| 9 | FMYCYFALV | Chiron consensus |
| 10 | SLVGFGILCV | Chiron consensus |
| 10 | SLMGCGLFWV | Chiron consensus |
| 8 | GLLGPLLV | HBVadr-ENV |
| 9 | AMAKAAAAI | A2.1 poly-A |
| 10 | MMWYWGPSLY | HBV |
| 9 | FLPSYFPSA | analog of 994.02: chiron comb |
| 9 | FAPSYFPSV | analog of 994.02: chiron comb |
| 9 | FLPSYFPSS | analog of 994.02: chiron comb |
| 9 | FSPSYFPSV | analog of 994.02: chiron comb |
| 9 | IMPKTGFLI | MAGE-1 |
| 9 | VADLVGFLL | MAGE-1 |
| 11 | EIWEELSVMEV | MAGE-1 |
| 11 | FLIIVLVMIAM | MAGE-1 |
| 11 | VIPHAMSSCGV | MAGE-1 |
| 11 | CILESCFRAVI | MAGE-1 |
| 9 | YIFATCLGL | MAGE3 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | YIFATCLGL | MAGE3 |
| 11 | KMVELVVHFLLL | MAGE2 112-122 |
| 11 | HLFIYATCLGL | MAGE3 174-184 |
| 9 | GLQDCTMLV | HCV NS5 2727-2735 |
| 8 | TLGIVSPI | HPV, analog of 1088.01 |
| 8 | TLGIVXPI | HPV, analog of 1088.01 |
| 10 | FLLAQFTSAI | HBV POL 513 |
| 11 | VLLDYQGMLPV | HBV env |
| 11 | CILLLCLIFLL | HBV env |
| 9 | FLGGSPVCL | HBV env |
| 11 | TVIEYLVSFGV | HBV core 114-124 |
| 11 | TVLEYLVSFGV | HBV core 114-124 |
| 10 | FLLAQFTSAI | HBV pol |
| 9 | GLYSSTVPI | HBV pol |
| 9 | GLYSSTAPI | HBV pol |
| 9 | GLDVLTAKV | HIV form VIN. |
| 9 | RILGAVAKV | HIV form VIN. |
| 9 | LLFGYPVYV | HTLV, tax 11-19 |
| 9 | ALFGYPVYV | tax 11-19, SAAS |
| 9 | LLFGAPVYV | tax 11-19, SAAS |
| 9 | LLFGYAVYV | tax 11-19, SAAS |
| 9 | LLFGYPVAV | tax 11-19, SAAS |
| 9 | AAGIGILTV | MART1 27-35 |
| 9 | GILTVILGV | MART1 31-39 |
| 9 | ILTVILGVL | MART1 32-40 |
| 9 | VILGVLLLI | MART1 35-43 |
| 9 | ALMDKSLHV | MART1 56-64 |
| 10 | TVILGVLLLI | MART1 |
| 10 | LLDGTATLRL | MART1 |
| 10 | ILSVSSFLFV | Plas. falcip. CSA-A 7-16 |
| 9 | GLIMVLSFL | Plas. falcip. CSA-A 401-409 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | IMVLSFLFL | Plas. falcip. CSA-A 403-411 |
| 10 | FLIFFDLFLV | Plas. falcip. TRAP-A 14-23 |
| 9 | FMKAVCVEV | Plas. falcip. TRAP-A 200-207 |
| 9 | IMPGQEAGL | gp100 |
| 9 | GLGQVPLIV | gp100 |
| 9 | LMAVVLASL | gp100 |
| 9 | RLMKQDFSV | gp100 |
| 9 | HLAVIGALL | gp100 |
| 9 | LLAVGATKV | gp100 |
| 9 | MLGTHTMEV | gp100 |
| 10 | LLDGTATLRL | gp100 |
| 10 | VLYRYGSFSV | gp100 |
| 10 | VLPSPACQLV | gp100 |
| 10 | SLADTNSLAV | gp100 |
| 10 | VLMAVVLASL | gp100 |
| 10 | LMAVVLASLI | gp100 |
| 10 | RLDCWRGGQV | gp100 |
| 10 | AMLGTHTMEV | gp100 |
| 10 | ALDGGNKHFL | gp100 |
| 9 | YLEPGPVTA | gp100 |
| 10 | LLNATAIAVA | |
| 11 | SLLNATAIAVA | |
| 9 | KTWGQYWQV | gp100 |
| 9 | ITDQVPFSV | gp100 |
| 9 | YLEPGPVTA | gp100 |
| 10 | LLDGTATLRL | gp100 |
| 10 | VLYRYGSFSV | gp100 |
| 10 | ALDGGNKHFL | gp100 |
| 9 | GILTVILGV | MART1 31-39 |
| 9 | YMNGTMSQV | Human Tyrosinase |
| 9 | MLLAVLYBL | Human Tyrosinase |
| 9 | LLWSFQTSA | Human Tyrosinase |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | YLTLAKHTI | Human Tyrosinase |
| 9 | FLPWHRLFL | Human Tyrosinase |
| 9 | FLLRWEQEI | Human Tyrosinase |
| 9 | RIWSWLLGA | Human Tyrosinase |
| 9 | LLGAAMVGA | Human Tyrosinase |
| 9 | AMVGAVLTA | Human Tyrosinase |
| 9 | VLTALLAGL | Human Tyrosinase |
| 9 | ALLAGLVSL | Human Tyrosinase |
| 9 | LLAGLVSLL | Human Tyrosinase |
| 10 | BLLWSFQTSA | Human Tyrosinase |
| 10 | WMHYYVSMDA | Human Tyrosinase |
| 10 | FLPWHRLFLL | Human Tyrosinase |
| 10 | WLLGAAMVGA | Human Tyrosinase |
| 10 | AMVGAVLTAL | Human Tyrosinase |
| 10 | VLTALLAGLV | Human Tyrosinase |
| 10 | TALLAGLVSL | Human Tyrosinase |
| 10 | ALLAGLVSLL | Human Tyrosinase |
| 9 | NLTDALLQV | P. falciparum SSP2 132 |
| 9 | SAWENVKNV | P. falciparum SSP2 218 |
| 10 | FLIFFDLFLV | P. falciparum SSP2 14 |
| 9 | NLNDNAIHL | P. falciparum SSP2 80 |
| 10 | YLLMDCSGSI | P. falciparum SSP2 51 |
| 9 | TLQDVSLEV | controls |

Table 11

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | ALYWFRTGI | HPV 6b/11 E1 319 |
| | LLDGNPMSI | HPV 6b/11 E1 540 |
| 9 | NAWGMVLLV | HPV 6b/11 E1 270 |
| 9 | SLYAHIQWL | HPV 6b/11 E1 260 |
| 9 | TLIKCPPLL | HPV 6b/11 E1 556 |
| 9 | GIYDALFDI | PSMAg 707 |
| 9 | YLSGANLNL | CEA 605 |
| 9 | VLYGPDTPI | CEA 589 |
| 9 | IMIGVLVGV | CEA 691 |
| 9 | LLTFWNPPT | CEA 24 |
| 9 | KLTEMVQWA | HPV 6b/11 E1 357 |
| 9 | YMDTYMRNL | HPV 6b/11 E1 532 |
| 10 | NLLDGNPMSI | HPV 6b/11 E1 539 |
| 10 | SLYAHIQWLT | HPV 6b/11 E1 260 |
| 10 | TLIKCPPLLV | HPV 6b/11 E1 556 |
| 10 | MVFELANSIV | PSMAg 583 |
| 10 | YLWWVNNQSL | CEA 176 |
| 10 | YLWWVNNQSL | CEA 354 |
| 10 | YLWWVNGQSL | CEA 532 |
| 10 | GIMIGVLVGV | CEA 690 |
| 10 | VLYGPDAPTI | CEA 233 |
| 10 | KLIEPLSLYA | HPV 6b/11 E1 254 |
| 10 | WLCAGALVLA | PSMAg 20 |
| 10 | IMIGVLVGVA | CEA 691 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | YLYQLSPPI | HTLV-I tax 155 |
| 9 | LLFEEYTNI | HTLV-I tax 307 |
| 9 | QLGAFLTNV | HTLV-I tax 178 |
| 9 | TLTAWQNGL | HTLV-I tax 226 |
| 9 | ALQFLIPRL | HTLV-I tax 67 |
| 9 | TLGQHLPTL | HTLV-I tax 123 |
| 9 | FAFKDLFVV | HPV 18 E6 47 |
| 9 | RLLQLLFRA | GCDFP-15 2 |
| 9 | CMVVKTYLI | GCDFP-15 65 |
| 9 | LLLVLCLQL | GCDFP-15 15 |
| 9 | ILYAHIQCL | HPV18 E1 266 |
| 9 | SLACSWGMV | HPV16 E1 266 |
| 9 | CLYLHIQSL | HPV16 E1 259 |
| 9 | YLVSPLSDI | HPV16 E1 90 |
| 9 | VMFLRYQGV | HPV16 E1 443 |
| 9 | KLLSKLLCV | HPV16 E1 292 |
| 9 | ALDGNPISI | HPV18 E1 546 |
| 9 | AVFKDTYGL | HPV18 E1 216 |
| 9 | LLTTNIHPA | HPV18 E1 570 |
| 9 | LLQQYCLYL | HPV16 E1 254 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | AMLAKFKEL | HPV16 E1 206 |
| 9 | ALDGNLVSM | HPV16 E1 539 |
| 9 | FLGALKSFL | HPV18 E1 463 |
| 9 | FIHFIQGAV | HPV18 E1 497 |
| 10 | TLLLVLCLQL | GCDFP-15 14 |
| 10 | LLFRASPATL | GCDFP-15 6 |
| 10 | SLMKFLQGSV | HPV16 E1 489 |
| 10 | SLACSWGMVV | HPV16 E1 266 |
| 10 | FLQGSVICFV | HPV16 E1 493 |
| 10 | FIQGAVISFV | HPV18 E1 500 |
| 10 | KLLCVSPMCM | HPV16 E1 296 |
| 10 | FILYAHIQCL | HPV18 E1 265 |
| 10 | FVNSTSHFWL | HPV18 E1 508 |
| 10 | ILLTTNIHPA | HPV18 E1 569 |
| 10 | TLLQQYCLYL | HPV16 E1 253 |
| 9 | GLLGWSPQA | HBV ENV 62 |
| 9 | GLACHQLCA | HER2/neu |
| 9 | ILDEAYVMA | HER2/neu |
| 9 | SIISAVVGI | HER2/neu |
| 9 | VVLGVVFGI | HER2/neu |
| 9 | YMIMVKCWM | HER2/neu |
| 10 | ALCRWGLLLA | HER2/neu |
| 10 | QLFEDNYALA | HER2/neu |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | HMWNFISGI | HCV consensus |
| 9 | VIYQYMDDL | HIV POL 358 |
| 9 | SLYNTVATL | HIV GAG 77 |
| 10 | TVWGIKQLQA | HIV ENV 735 |
| 9 | LLLEAGALV | MSH 99 |
| 9 | VLETAVGLL | MSH 92 |
| 9 | CLALSDLLV | MSH 79 |
| 9 | FLSLGLVSL | MSH 45 |
| 9 | SLVENALVV | MSH 52 |
| 9 | AIIDPLIYA | MSH 291 |
| 9 | FLCWGPFFL | MSH 251 |
| 9 | FLALIICNA | MSH 283 |
| 9 | TILLGIFFL | MSH 244 |
| 9 | RLLGSLNST | MSH 9 |
| 9 | SLYNTVATL | HIV p17/5B 77-8 |
| 9 | VIYQYMDDL | HIV RT/50A 346- |
| 9 | ILKEPVHGV | HIV RT/IV9 476- |

Table 12

| PEPTIDE NO. | PEPTIDE LENGTH | SEQUENCE |
|---|---|---|
| 1237.01 | 9 | FLWGPQALV |
| 1237.02 | 9 | FLWGPNALV |
| 1237.03 | 9 | FLWGPHALV |
| 1237.04 | 9 | FLWGPKALV |
| 1237.05 | 9 | FLWGPFALV |
| 26.0158 | 9 | AVIGALLAV |
| 26.0172 | 9 | LLHLAVIGA |
| 26.0186 | 9 | SLADTNSLA |
| 26.0192 | 9 | VMGTTLAEM |
| 26.0240 | 9 | LLAVLYCLL |
| 26.0383 | 10 | FLRNQPLTFA |
| 26.0390 | 10 | HLAVIGALLA |
| 26.0395 | 10 | LAVIGALLAV |
| 26.0418 | 10 | TLAEMSTPEA |
| 26.0423 | 10 | YLAEADLSYT |
| 26.0497 | 10 | MLLAVLYCLL |
| 1183.10 | 10 | VLYRYGSFSV |
| 27.0007 | 9 | ILSSLGLPV |
| 27.0012 | 9 | LLFLGVVFL |
| 27.0019 | 9 | GLYGAQYDV |
| 27.0022 | 9 | FVVALIPLV |
| 27.0023 | 9 | GLMTAVYLV |
| 27.0027 | 9 | ALVLLMLPV |
| 27.0028 | 9 | ILLSIARVV |
| 27.0029 | 9 | SLYFGGICV |
| 27.0030 | 9 | QLIPCMDVV |
| 27.0031 | 9 | VLQQSTYQL |
| 27.0032 | 9 | AIHNVVHAI |
| 27.0034 | 9 | GLHGVGVSV |
| 27.0035 | 9 | GLVDFVKHI |
| 27.0036 | 9 | LLFRFMRPL |
| 27.0038 | 9 | LMLPGMNGI |
| 27.0043 | 9 | TVLRFVPPL |
| 27.0044 | 9 | MLGNAPSVV |
| 27.0050 | 9 | YLDLALMSV |
| 27.0064 | 9 | RMPEAAPPV |

| PEPTIDE NO. | PEPTIDE LENGTH | SEQUENCE |
|---|---|---|
| 27.0082 | 9 | FLLPDAQSI |
| 27.0083 | 9 | MTYAAPLFV |
| 27.0088 | 9 | LLPLGYPFV |
| 27.0089 | 9 | GLYYLTTEV |
| 27.0090 | 9 | MALLRLPLV |
| 27.0091 | 9 | RLPLVLPAV |
| 27.0093 | 9 | RMFAANLGV |
| 27.0095 | 9 | RLLDDTPEV |
| 27.0096 | 9 | YLYVHSPAL |
| 27.0100 | 9 | GLYLSQIAV |
| 27.0101 | 9 | YLSQIAVLL |
| 27.0102 | 9 | SLAGFVRML |
| 27.0137 | 10 | ATYDKGILTV |
| 27.0146 | 10 | KIFMLVTAVV |
| 27.0151 | 10 | FLLADERVRV |
| 27.0153 | 10 | MLATDLSLRV |
| 27.0154 | 10 | RLQPQVGWEV |
| 27.0161 | 10 | FLMPVEDVFI |
| 27.0165 | 10 | RMSRVTTFTV |
| 27.0168 | 10 | LALVLLMLPV |
| 27.0169 | 10 | ALVLLMLPVV |
| 27.0170 | 10 | GIVSGILLSI |
| 27.0171 | 10 | SLYFGGICVI |
| 27.0173 | 10 | QLIPCMDVVL |
| 27.0181 | 10 | LLFRFMRPLI |
| 27.0183 | 10 | VLLEDGGVEV |
| 27.0184 | 10 | AMPAYNWMTV |
| 27.0186 | 10 | GLAGTVLRFV |
| 27.0188 | 10 | VLIAFGRFPI |
| 27.0189 | 10 | FLTCDANLAV |
| 27.0197 | 10 | AIAWGAWGEV |
| 27.0204 | 10 | LLLETSWEAI |
| 27.0217 | 10 | RMPEAAPPVA |
| 27.0223 | 10 | WMAETTLGRV |
| 27.0226 | 10 | AMALLRLPLV |
| 27.0229 | 10 | FMSLAGFVRM |
| 27.0266 | 11 | SLLTEVETYVL |

| PEPTIDE NO. | PEPTIDE LENGTH | SEQUENCE |
|---|---|---|
| 27.0268 | 11 | GILGFVFTLTV |
| 27.0269 | 11 | VLDVGDAYFSV |
| 27.0271 | 11 | KIWEELSMLEV |
| 27.0272 | 11 | STLVEVTLGEV |
| 27.0273 | 11 | GLAPPQHLIRV |
| 27.0274 | 11 | HLIRVEGNLRV |
| 27.0005 | 9 | YLLALRYLA |
| 27.0013 | 9 | GLYRQWALA |
| 27.0017 | 9 | LLWQDPVPA |
| 27.0040 | 9 | ALLSDWLPA |
| 27.0045 | 9 | WLLIDTSNA |
| 27.0046 | 9 | MLASTLTDA |
| 27.0081 | 9 | YLSEGDMAA |
| 27.0094 | 9 | LLACAVIHA |
| 27.0144 | 10 | LLCCSGVATA |
| 27.0191 | 10 | LLATVFKLTA |
| 27.0192 | 10 | KLTADGVLTA |
| 27.0195 | 10 | GLGGLGLFFA |
| 28.0064 | 8 | TLGIVXPI |
| 28.0065 | 8 | ALGTTXYA |
| 28.0293 | 9 | FLLTRILTV |
| 28.0294 | 9 | ALMPLYACV |
| 28.0295 | 9 | LLAQFTSAV |
| 28.0296 | 9 | LLPFVQWFV |
| 28.0297 | 9 | FLLAQFTSV |
| 28.0298 | 9 | KLHLYSHPV |
| 28.0299 | 9 | KLFLYSHPI |
| 28.0300 | 9 | LLSSNLSWV |
| 28.0301 | 9 | FLLSLGIHV |
| 28.0302 | 9 | MMWYWGPSV |
| 28.0303 | 9 | VLQAGFFLV |
| 28.0304 | 9 | PLLPIFFCV |
| 28.0305 | 9 | FLLPIFFCL |
| 28.0306 | 9 | VLLDYQGMV |
| 28.0307 | 9 | YMDDVVLGV |
| 28.0308 | 9 | YMFDVVLGA |
| 28.0309 | 9 | GLLGWSPQV |

| PEPTIDE NO. | PEPTIDE LENGTH | SEQUENCE |
|---|---|---|
| 28.0342 | 9 | YMIMVKXWM |
| 28.0343 | 9 | YIFATXLGL |
| 28.0345 | 9 | SLHXKPEEA |
| 28.0346 | 9 | ALGLVXVQA |
| 28.0348 | 9 | LLMDXSGSI |
| 28.0349 | 9 | FAFRDLXIV |
| 28.0352 | 9 | GTLGIVXPI |
| 28.0353 | 9 | TLGIVXPIX |
| 28.0354 | 9 | LLWFHISXL |
| 28.0355 | 9 | KLTPLXVTL |
| 28.0356 | 9 | ALVEIXTEM |
| 28.0357 | 9 | LTFGWXFKL |
| 28.0359 | 9 | KLQXVDLHV |
| 28.0360 | 9 | FMKAVXVEV |
| 28.0361 | 9 | LLQQYXLYL |
| 28.0362 | 9 | XLYLHIQSL |
| 28.0363 | 9 | SLAXSWGMV |
| 28.0364 | 9 | ILYAHIQXL |
| 28.0365 | 9 | KLLSKLLXV |
| 28.0366 | 9 | PLLPIFFXL |
| 28.0367 | 9 | TLIKXPPLL |
| 28.0368 | 9 | ALMPLYAXI |
| 28.0370 | 9 | XILESLFRA |
| 28.0609 | 10 | FLLAQFTSAV |
| 28.0610 | 10 | YLHTLWKAGV |
| 28.0611 | 10 | YLFTLWKAGI |
| 28.0612 | 10 | YLLTLWKAGI |
| 28.0613 | 10 | LLFYQGMLPV |
| 28.0614 | 10 | LLLYQGMLPV |
| 28.0615 | 10 | LLVLQAGFFV |
| 28.0616 | 10 | ILLLCLIFLV |
| 28.0650 | 10 | ALXRWGLLL |
| 28.0651 | 10 | KLPDLXTEL |
| 28.0652 | 10 | HLYQGXQVV |
| 28.0653 | 10 | XILESLFRA |
| 28.0654 | 10 | KLQXVDLHV |
| 28.0655 | 10 | YIFATXLGL |

| PEPTIDE NO. | PEPTIDE LENGTH | SEQUENCE |
|---|---|---|
| F111.01 | 9 | SLYNTVATL |
| F111.02 | 9 | ALYNTVATL |
| F111.04 | 9 | SLANTVATL |
| F111.06 | 9 | SLFNAVATL |
| F111.07 | 9 | SLFNLLATL |
| F111.10 | 9 | SLFNTIAVL |
| F111.11 | 9 | SLFNAVAVL |
| F111.09 | 9 | SLFNTIVVL |
| F111.12 | 9 | SLFNAIAVL |
| F111.13 | 9 | SLFNTVAVL |
| F111.14 | 9 | SLFNTVCVI |
| F111.15 | 9 | SLHNTVATL |
| F111.17 | 9 | SLHNTVAVL |
| F111.18 | 9 | SLYATVATL |
| F111.19 | 9 | SLYNAVATL |
| F111.21 | 9 | SLYNTAATL |
| F111.22 | 9 | SLYNTIAVL |
| F111.23 | 9 | SLYNTSATL |
| F111.25 | 9 | SLYNTVAVL |
| F111.26 | 9 | SLYNTVATA |
| F111.27 | 9 | SLYNAIATL |
| F111.28 | 9 | SLYNLVAVL |
| F111.29 | 9 | SLFNLLAVL |
| F111.32 | 9 | SLFNTVVTL |
| F111.34 | 9 | SLYNTVAAL |
| 1039.031 | 9 | MMWYWGPSL |
| 1211.40 | 10 | SLLNATAIAV |
| | 10 | TIHDIILECV |
| | 9 | FAFRDLCIV |
| | 9 | GTLGIVCPI |
| | 9 | TLGIVCPIC |

Table 13

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | IPQSLDSWW | HBV ENV 191 |
| 9 | IPIPSSWAF | HBV ENV 313 |
| 9 | TPARVTGGV | HBV POL 365 |
| 9 | LPIFFCLWV | HBV ENV 379 |
| 9 | HPAAMPHLL | HBV POL 440 |
| 9 | FPHCLAFSY | HBV POL 541 |
| 9 | DPSRGRLGL | HBV POL 789 |
| 9 | QPRGRRQPI | HCV Core 57 |
| 9 | SPRGSRPSW | HCV Core 99 |
| 9 | DPRRRSRNL | HCV Core 111 |
| 9 | LPGCSFSIF | HCV Core 168 |
| 9 | YPCTVNFTI | HCV E2 622 |
| 9 | LPALSTGLI | HCV E2 681 |
| 9 | HPNIEEVAL | HCV NS3 1358 |
| 9 | SPGALVVGV | HCV NS4 1887 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | SPGQRVEFL | HCV NS5 2615 |
| 9 | APTLWARMI | HCV NS5 2835 |
| 9 | FPRIWLHJL | HIV VPR 34 |
| 9 | SPTRRELQV | HIV POL 37 |
| 9 | FPVRPQVPL | HIV NEF 84 |
| 9 | RPQVPLRPM | HIV NEF 87 |
| 9 | KPCVKLTPL | HIV ENV 123 |
| 9 | SPRTLNAWV | HIV GAG 153 |
| 9 | FPISPIETV | HIV POL 171 |
| 9 | SPAIFQSSM | HIV POL 327 |
| 9 | NPDIVIYQY | HIV POL 346 |
| 9 | GPGHKARVL | HIV GAG 360 |
| 9 | LPEKDSWTV | HIV POL 417 |
| 9 | YPLASLRSL | HIV GAG 507 |
| 9 | VPRRKAKII | HIV POL 991 |
| 9 | TPTLHEYML | HPV16 E7 5 |
| 9 | KPLNPAEKL | HPV18 E6 110 |
| 9 | NPAEKLRHL | HPV18 E6 113 |
| 9 | VPISHLYIL | MAGE2 170 |
| 9 | MPKTGLLII | MAGE2 196 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | DPACYEFLW | MAGE2 265 |
| 9 | EPHISYPPL | MAGE2 296 |
| 9 | YPPLHERAL | MAGE2 301 |
| 9 | LPTTMNYPL | MAGE3 71 |
| 9 | DPIGHLYIF | MAGE3 170 |
| 9 | MPKAGLLII | MAGE3 196 |
| 9 | GPHISYPPL | MAGE3 296 |
| 9 | HPSDGKCNL | P. falciparum S |
| 9 | RPRGDNFAV | P. falciparum S |
| 9 | QPRPRGDNF | P. falciparum S |
| 9 | LPNDKSDRY | P. falciparum S |
| 10 | LPLDKGIKPY | HBV POL 123 |
| 10 | TPARVTGGVF | HBV POL 365 |
| 10 | FPHCLAFSYM | HBV POL 541 |
| 10 | LPRRGPRLGV | HCV Core 37 |
| 10 | APLGGAARAL | HCV Core 142 |
| 10 | LPGCSFSIFL | HCV Core 168 |
| 10 | VPASQVCGPV | HCV E2 497 |
| 10 | YPCTVNFTIF | HCV E2 622 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | SPLLLSTTEW | HCV E2 663 |
| 10 | RPSGMFDSSV | HCV NS3 1506 |
| 10 | LPVCQDHLEF | HCV NS3 1547 |
| 10 | KPTLHGPTPL | HCV NS3 1614 |
| 10 | TPLLYRLGAV | HCV NS3 1621 |
| 10 | NPAIASLMAF | HCV NS4 1783 |
| 10 | LPAILSPGAL | HCV NS4 1882 |
| 10 | SPGALVVGVV | HCV NS4 1887 |
| 10 | APTLWARMIL | HCV NS5 2835 |
| 10 | IPVGEIYKRW | HIV GAG 261 |
| 10 | YPLASLRSLF | HIV GAG 507 |
| 10 | APTKAKRRVV | HIV ENV 547 |
| 10 | VPISHLYILV | MAGE2 170 |
| 10 | MPKTGLLIIV | MAGE2 196 |
| 10 | HPRKLLMQDL | MAGE2 241 |
| 10 | LPTTMNYPLW | MAGE3 71 |
| 10 | MPKAGLLIIV | MAGE3 196 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | IPYSPLSPKV | P. falciparum S |
| 10 | TPYAGEPAPF | P. falciparum S |
| 9 | FPDHQLDPA | HBV ENV 14 |
| 9 | YPALMPLYA | HBV POL 640 |
| 9 | LPVCAFSSA | HBV X 58 |
| 9 | APLGGAARA | HCV 142 |
| 9 | DPTTPLARA | HCV 2806 |
| 9 | FPYLVAYQA | HCV 1582 |
| 9 | LPAILSPGA | HCV 1882 |
| 9 | NPAIASLMA | HCV 1783 |
| 9 | TPIDTTIMA | HCV 2551 |
| 9 | TPLLYRLGA | HCV 1621 |
| 9 | WPLLLLLLA | HCV 793 |
| 9 | NPYNTPVFA | HIV POL 225 |
| 9 | APLLLARAA | PAP 4 |
| 9 | HPQWVLTAA | PSA 52 |
| 10 | IPIPSSWAFA | HBV ENV 313 |
| 10 | TPPAYRPPNA | HBV NUC 128 |
| 10 | APFTQCGYPA | HBV POL 633 |
| 10 | LPIHTAELLA | HBV POL 712 |
| 10 | GPCALRFTSA | HBV X 67 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | DPTTPLARAA | HCV 2806 |
| 10 | IPQAVVDMVA | HCV 339 |
| 10 | LPCSFTTLPA | HCV 674 |
| 10 | QPEKGGRKPA | HCV 2567 |
| 10 | VPHPNIEEVA | HCV 1356 |
| 10 | IPAETGQETA | HIV POL 820 |
| 10 | LPQGWKGSPA | HIV POL 320 |
| 10 | FPDLESEFQA | MAGE2/3 98 |
| 10 | DPIGHLYIFA | MAGE3 170 |
| 9 | EPLSLYAHI | HPV 6b/11 E1 2 |
| 9 | PPLLVTSNI | HPV 6b/11 E1 5 |
| 9 | SPRLDAIKL | HPV 6b/11 E1 1 |
| 9 | TPKKNCIAI | HPV 6b/11 E1 4 |
| 9 | FPFDRNGNA | HPV 6b/11 E1 5 |
| 10 | CPPLLVTSNI | HPV 6b/11 E1 5 |
| 10 | FPFDRNGNAV | HPV 6b/11 E1 5 |
| 8 | GPLLVLQA | HBV ENV 173 |
| 8 | IPIPSSWA | HBV ENV 313 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 8 | VPFVQWFV | HBV ENV 340 |
| 8 | LPIFFCLW | HBV ENV 379 |
| 8 | RPPNAPIL | HBV NUC 133 |
| 8 | MPLSYQHF | HBV POL 1 |
| 8 | HPAAMPHL | HBV POL 429 |
| 8 | SPFLLAQF | HBV POL 511 |
| 8 | YPALMPLY | HBV POL 640 |
| 8 | SPTYKAFL | HBV POL 659 |
| 8 | VPSALNPA | HBV POL 769 |
| 8 | HPvhAGPI | HIV con. GAG |
| 8 | GPGvRyPL | HIV con. NEF |
| 8 | SPIETVPV | HIV con. POL |
| 8 | NPYNTPVF | HIV con. POL |
| 8 | LPIQKETW | HIV con. POL |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 8 | VPRRKaKi | HIV con. POL |
| 8 | VpLQLPPl | HIV con. REV |
| 8 | VPLAMKLI | P. falciparum |
| 8 | LPYGRTNL | P. falciparum |
| 8 | RPRGDNFA | P. falciparum |
| 8 | IPQQEPNI | P. falciparum |
| 8 | TPFAGEPA | P. falciparum |
| 9 | SPINTIAEA | HPV 6b E1 93 |
| 9 | SPISNVANA | HPV 11 E1 93 |
| 9 | SPRLDAIKL | HPV 6b/11 E1 1 |
| 9 | EPLSLYAHI | HPV 6b/11 E1 2 |
| 9 | EPPKIQSGV | HPV 6b/11 E1 3 |
| 9 | IPFLTKFKL | HPV 6b E1 455 |
| 9 | TPKKNCIAI | HPV 6b/11 E1 4 |
| 9 | QPLTDAKVA | HPV 11 E1 512 |
| 9 | PPLLVTSNI | HPV 6b/11 E1 5 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | FPFDRNGNA | HPV 6b/11 E1 5 |
| 9 | APLILSRIV | PSA 14 |
| 9 | HPEDTGQVF | PSA 78 |
| 9 | HPLYDMSLL | PSA 94 |
| 9 | HPQKVTKFM | PSA 184 |
| 9 | GPLVCNGVL | PSA 211 |
| 9 | RPSLYTKVV | PSA 235 |
| 9 | FPPEGVSIW | PAP 124 |
| 9 | NPILLWQPI | PAP 133 |
| 9 | LPFRNCPRF | PAP 156 |
| 9 | IPSYKKLIM | PAP 277 |
| 9 | LPPYASCHL | PAP 307 |
| 9 | SPSCPLERF | PAP 348 |
| 9 | CPLERFAEL | PAP 351 |
| 9 | GPTLIGANA | gp100 74 |
| 9 | LPDGQVIWV | gp100 97 |
| 9 | VPLAHSSSA | gp100 198 |
| 9 | QPLTFALQL | gp100 236 |
| 9 | DPSGYLAEA | gp100 246 |
| 9 | EPGPVTAQV | gp100 282 |
| 9 | MPTAESTGM | gp100 366 |
| 9 | TPAEVSIVV | gp100 401 |
| 9 | LPKEACMEI | gp100 520 |
| 9 | LPSPACQLV | gp100 545 |
| 9 | VPLIVGILL | gp100 596 |
| 9 | LPHSSSHWL | gp100 630 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | CPIGENSPL | gp100 647 |
| 9 | SPLLSGQQV | gp100 653 |
| 9 | MPREDAHFI | MART1 1 |
| 9 | APLGPQFPF | Tyrosinase 6 |
| 9 | IPIGTYGQM | Tyrosinase 1 |
| 9 | TPMFNDINI | Tyrosinase 1 |
| 9 | LPWHRLFLL | Tyrosinase 2 |
| 9 | IPYWDWRDA | Tyrosinase 2 |
| 9 | SPASFFSSW | Tyrosinase 2 |
| 9 | LPSSADVEF | Tyrosinase 3 |
| 9 | SPLTGIADA | Tyrosinase 3 |
| 9 | DPIFLLHHA | Tyrosinase 3 |
| 9 | IPLYRNGDF | Tyrosinase 4 |
| 9 | YPELPKPSI | CEA 141 |
| 9 | LPVSPRLQL | CEA 185 |
| 9 | LPVSPRLQL | CEA 363 |
| 9 | NPPAQYSWL | CEA 442 |
| 9 | LPVSPRLQL | CEA 541 |
| 9 | IPQQHTQVL | CEA 632 |
| 9 | NPPAQYSWF | CEA 264 |
| 9 | LPSIPVHPI | Prost.Ca PSM |
| 9 | IPVHPIGYY | Prost.Ca PSM |
| 9 | RPFYRHVIY | Prost.Ca PSM |
| 9 | TPKHNMKAF | Prost.Ca PSM |
| 9 | FPGIYDALF | Prost.Ca PSM |
| 9 | RPRWLCAGA | Prost.Ca PSM |
| 9 | DPLTPGYPA | Prost.Ca PSM |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | RPRRTILFA | Prost.Ca PSM |
| 9 | LPFDCRDYA | Prost.Ca PSM |
| 9 | LPIHTAELL | HBV POL 712 |
| 10 | GPDAPTISPL | CEA 236 |
| 10 | IPQQHTQVLF | CEA 632 |
| 10 | QPIPVHTVPL | Prost.Ca PAP |
| 10 | HPYKDFIATL | Prost.Ca PAP |
| 10 | LPGCSPSCPL | Prost.Ca PAP |
| 10 | LPSWATEDTM | Prost.Ca PAP |
| 10 | VPLSEDQLLY | Prost.Ca PAP |
| 10 | FPHPLYDMSL | Prost.Ca PSA |
| 10 | RPGDDSSHDL | Prost.Ca PSA |
| 10 | HPQKVTKFML | Prost.Ca PSA |
| 10 | LPFDCRDYAV | Prost.Ca PSM |
| 10 | YPNKTHPNYI | Prost.Ca PSM |
| 10 | SPEFSGMPRI | Prost.Ca PSM |
| 10 | RPRWLCAGAL | Prost.Ca PSM |
| 10 | TPKHNMKAFL | Prost.Ca PSM |
| 10 | RPFYRHVIYA | Prost.Ca PSM |
| 10 | HPAAMPHLLV | HBV POL 429 |
| 9 | SPREGPLPA | HER2/neu 1151 |
| 9 | KPDLSYMPI | HER2/neu 605 |
| 9 | HPPPAFSPA | HER2/neu 1208 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | GPLPAARPA | HER2/neu 1155 |
| 9 | APQPHPPPA | HER2/neu 1204 |
| 9 | EPLTPSGAM | HER2/neu 698 |
| 9 | LPTHDPSPL | HER2/neu 1101 |
| 9 | DPLNNTTPV | HER2/neu 121 |
| 9 | SPLTSIISA | HER2/neu 649 |
| 9 | SPKANKEIL | HER2/neu 760 |
| 9 | LPTNASLSF | HER2/neu 65 |
| 9 | CPSGVKPDL | HER2/neu 600 |
| 9 | SPLAPSEGA | HER2/neu 1073 |
| 9 | MPNQAQMRI | HER2/neu 706 |
| 9 | LPAARPAGA | HER2/neu 1157 |
| 9 | LPQPPICTI | HER2/neu 941 |
| 9 | SPAFDNLYY | HER2/neu 1214 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | TPTAENPEY | HER2/neu 1240 |
| 9 | LPSETDGYV | HER2/neu 1120 |
| 10 | LPTNASLSFL | HER2/neu 65 |
| 10 | CPAEQRASPL | HER2/neu 642 |
| 10 | KPCARVCYGL | HER2/neu 336 |
| 10 | APQPHPPPAF | HER2/neu 1204 |
| 10 | SPGGLRELQL | HER2/neu 133 |
| 10 | SPLTSIISAV | HER2/neu 649 |
| 10 | MPNQAQMRIL | HER2/neu 706 |
| 10 | SPYVSRLLGI | HER2/neu 779 |
| 10 | HPPPAFSPAF | HER2/neu 1208 |
| 10 | SPREGPLPAA | HER2/neu 1151 |
| 10 | NPHQALLHTA | HER2/neu 488 |
| 10 | MPYGCLLDHV | HER2/neu 801 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 10 | GPASPLDSTF | HER2/neu 995 |
| 9 | LPTTLFQPV | HTLV-I tax 21 |
| 9 | IPPSFLQAM | HTLV-I tax 10 |
| 9 | FPGFGQSLL | HTLV-I tax 4 |
| 9 | WPLLPHVIF | HTLV-I tax 16 |
| 9 | SPPITWPLL | HTLV-I tax 16 |
| 9 | VPYKRIEEL | HTLV-I tax 18 |
| 9 | RPQNLYTLW | HTLV-I tax 13 |
| 9 | CPKDGQPSL | HTLV-I tax 26 |
| 9 | RPNDEVTAV | GCDFP-15 47 |
| 9 | SPATLLLVL | GCDFP-15 11 |
| 9 | WPYLHNRLV | HPV16 E1 576 |
| 9 | QPFILYAHI | HPV18 E1 263 |
| 9 | SPRLKAICI | HPV16 E1 107 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | SPLGERLEV | HPV18 E1 97 |
| 9 | SPRLQEISL | HPV18 E1 110 |
| 9 | RPIVQFLRY | HPV18 E1 447 |
| 10 | WPYLHNRLVV | HPV16 E1 576 |
| 10 | WPYLESRITV | HPV18 E1 583 |
| 10 | QPPKLRSSVA | HPV18 E1 315 |
| 10 | EPPKLRSTAA | HPV16 E1 308 |
| 9 | DPSRGRLGL | HBV POL 778 |
| 9 | HPAAMPHLL | HBV POL 429 |
| 9 | IPIPSSWAF | HBV ENV 313 |
| 10 | TPARVTGGVF | HBV POL 354 |
| 10 | FPHCLAFSYM | HBV POL 530 |
| 9 | LPVCAFSSA | HBV X 58 |
| 9 | YPALMPLYA | HBV POL 640 |
| 9 | APLLLARAA | PAP 4 |

| AA | SEQUENCE | SOURCE |
|---|---|---|
| 9 | HPQWVLTAA | PSA 52 |
| 9 | HPSDGKCNL | Pf SSP2 206 |
| 9 | RPRGDNFAV | Pf SSP2 305 |
| 9 | QPRPRGDNF | Pf SSP2 303 |
| 10 | TPYAGEPAPF | Pf SSP2 539 |
| 9 | GPHISYPPL | MAGE3 296 |
| 9 | YPPLHERAL | MAGE2 301 |
| 9 | VPISHLYIL | MAGE2 170 |
| 9 | EPHISYPPL | MAGE2 296 |
| 9 | LPTTMNYPL | MAGE3 71 |
| 9 | MPKAGLLII | MAGE3 196 |
| 10 | HPRKLLMQDL | MAGE2 241 |

Table 14

| PEPTIDE | AA | SEQUENCE |
|---|---|---|
| 25.0129 | 9 | LPPLERLTL |
| 26.0445 | 10 | EPGPVTAQVV |
| 26.0448 | 10 | LPRIFCSCPI |
| 26.0449 | 10 | LPSPACQLVL |
| 26.0455 | 10 | VPLAHSSSAF |
| 26.0458 | 10 | VPRNQDWLGV |
| 26.0476 | 10 | APPAYEKLSA |
| 26.0478 | 10 | MPREDAHFIY |
| 26.0519 | 10 | APAFLPWHRL |
| 26.0522 | 10 | GPNCTERRLL |
| 26.0523 | 10 | IPLYRNGDFF |
| 26.0529 | 10 | TPRLPSSADV |
| 19.0101 | 9 | TPAEVSIVV |
| 26.0554 | 11 | APFTQCGYPAL |
| 26.0561 | 11 | NPADDPSRGRL |
| 26.0564 | 11 | RPPNAPILSTL |
| 26.0566 | 11 | SPFLLAQFTSA |
| 26.0567 | 11 | SPHHTALRQAI |
| 26.0568 | 11 | TPARVTGGVFL |

WHAT IS CLAIMED IS:

1. A composition comprising an immunogenic peptide having an HLA binding motif, which immunogenic peptide is a peptide shown in Tables 3-14 or a peptide comprising a conservative substitution of a residue in a peptide shown in Table 3-14.

2. The composition of claim 1, wherein the immunogenic peptide is linked to a second oligopeptide.

3. The composition of claim 2, wherein the second oligopeptide is a peptide that induces a helper T response.

4. A composition comprising a nucleic acid molecule encoding an immunogenic peptide as shown in Tables 3-14, or a peptide comprising a conservative substitution of a residue of a peptide shown in Table 3-14.

5. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding a second immunogenic peptide.

6. The composition of claim 4, wherein the nucleic acid further comprises a sequence encoding an oligopeptide that induces a helper T response.

7. A method of inducing a cytotoxic T cell response comprising contacting a cytotoxic T cell with a peptide of claim 1.

# INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

A. CLASSIFICATION OF SUBJECT MATTER
IPC(6) :A61K 39/00, 39/29; C07K 7/00, 14/02, 14/82
US CL : 424/185.1; 530/300, 328, 350
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/185.1; 530/300, 328, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

STN file=reg of first sequence in Table 3. Examiner's MHC/peptide files.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN file=reg sequence search of first sequence in Table 3. STN file=ca of hits on sequence search.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| T | BRUSS, V. A short linear sequence in the pre-S domain of the large hepatitis B virus envelope protein required from virion formation. J. Virology. December 1997, Vol. 71, No. 12, pages 9350-9357. See entire document | 1-3 and 7 |
| Y | PREISLER-ADAMS, S. et al. Complete nucleotide sequence of a hepatitis B virus, subtype adw2, and identification of three types of C open reading frame. Nucleic Acids Res. 1993, Vol. 21, No. 9, page 2258. See entire document. | 1-3 and 7 |
| Y | RAMMENSEE, H. et al. Peptides naturally presented by MHC Class I molecules. Annu. Rev. Immunol. 1993, Vol. 11, pages 213-243, see entire article. | 1-3 and 7 |

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

| | | | |
|---|---|---|---|
| * | Special categories of cited documents: | "T" | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| "A" | document defining the general state of the art which is not considered to be of particular relevance | "X" | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| "E" | earlier document published on or after the international filing date | "Y" | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| "L" | document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | "&" | document member of the same patent family |
| "O" | document referring to an oral disclosure, use, exhibition or other means | | |
| "P" | document published prior to the international filing date but later than the priority date claimed | | |

Date of the actual completion of the international search
12 MAY 1998

Date of mailing of the international search report
17 JUL 1998

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231
Facsimile No. (703) 305-3230

Authorized officer
THOMAS CUNNINGHAM
Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| Y | ENGELHARD, V. et al. Structure of peptides associated with MHC Class I molecules. Curr. Opin. Immunol. 1994, Vol. 6, pages 13-23, see entire document. | 1-3 and 7 |

# INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

See attached sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-3 and 7

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/05039

Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
1. This International Search Authority has found 3453 inventions claimed in the International Application covered by the claims indicated below:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-3 and 7, drawn to compositions comprising peptides and methods of inducing CTL responses using such compositions. A review of Tables 3-14 indicates there are 2764 structurally different peptides recited.

Group II, claim(s) 4-6, drawn to nucleic acids encoding peptides. Claims 4-6 recite nucleic acids encoding the 2764 different peptides of Tables 3-14.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. The species are as follows:

Each of the 2764 different peptides recited by Tables 3-14 and each of the 2764 different nucleic acid sequences encoding the peptides of Tables 3-14. 2764 + 2764 = 5,528 total species.

The claims are deemed to correspond to the species listed above in the following manner:

The following claims are generic: claims 1-7 because they encompass all of the peptides or nucleic acid sequences encoding the peptides of Tables 3-14.

The first peptide species recited in Table 3 (FTF. . .LSK) will be examined. Each additional peptide species requires the payment of a separate fee. To have all the recited peptide species searched requires the payment of 2763 additional fees.

Upon payment for Group II, the Office will examine the first ten (or ten that the Applicant selects) nucleic acid species at no additional cost. Each four species of nucleic acids thereafter requires the payment of a separate fee. To have all the nucleic acid species searched requires the payment of (2764-10)/4 = 689 additional fees.

and it considers that the International Application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for the reasons indicated below:

The inventions listed as Groups I and II do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the peptides of Group I lack the corresponding technical structural and functional features of the nucleic acids of Group II.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: the 5528 different species of peptides recited by Tables 3-14 (or the nucleic acid sequences encoding such peptides) lack the same or corresponding special technical features of common structure and function, source of isolation and amino acid or nucleic acid identity. Each separate species would require a separate prior art search.